

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 14:47:45 ; Search time 2250 Seconds
(without alignments)
6240.661 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867

Sequence: 1 agctactcagagagctgaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110.8	12.8	466	17	AQ229478 HS.2021.A
2	109.2	12.6	680	17	AG186502 Pan. trogl
3	107.6	12.4	418	17	AQ390169 CITR1-El-
4	107.2	12.4	469	13	BM509394 Ih17.F10.Y
5	107.2	12.4	516	13	BI468297 Id87.B01.Y
6	107.2	12.4	529	14	BQ270800 IK05b06.Y

Result No.	Score	Query Match	Length	DB ID	Description
7	107.2	12.4	556	14	BQ267333 IK02c03.Y
8	107.2	12.4	589	14	BQ270346 IK09g10.Y
9	106.4	12.3	635	17	AQ428429 CITR1-El-
10	106	12.2	774	17	AQ751486 HS.5576.B
11	104.8	12.1	671	17	AQ418931 RPl-11-1
12	104.6	12.1	465	17	AQ527107 CITR1-El-
13	104.4	12.0	815	14	BQ429052 AGENCOURT
14	104.4	12.0	303	14	BM672404 UI-E-COO-
15	104.4	12.0	712	17	AG139751 Pan. trogl
16	103.8	12.0	451	14	M66929
17	103	11.9	837	13	BI820230
18	103	11.9	1074	14	BQ429712
19	102.8	11.9	318	13	BI492686
20	102.8	11.9	340	10	AM021747
21	102.8	11.9	684	17	AG109444 Pan. trogl
22	102	11.8	364	17	AQ333390
23	101.6	11.7	256	9	AA084337
24	101.2	11.7	382	10	AV764523
25	101.2	11.7	474	9	AI866580
26	101.2	11.7	514	17	B37536
27	101.2	11.7	735	9	AU120382
28	101.2	11.7	773	12	BG221771 RST41586
29	101.2	11.7	815	12	BF382750
30	101.2	11.7	859	17	AQ750588 HS.5573.B
31	101.2	11.7	925	12	BG249993
32	101	11.6	445	17	AQ198078
33	100.4	11.6	504	9	AI138096
34	100.2	11.6	335	9	AA492202
35	100	11.5	459	17	AQ483064
36	99.8	11.5	404	14	W07861
37	99.8	11.5	460	9	AI597733
38	99.8	11.5	464	10	AM150226
39	99.8	11.5	662	17	AQ262070
40	99.8	11.5	712	9	AL709370 CITR1-El-
41	99.6	11.5	238	17	AQ344289
42	99.6	11.5	281	9	AI453660
43	99.6	11.5	419	17	AQ036584 CIT-HSP-2
44	99.6	11.5	494	12	BF916367
45	99.6	11.5	1661	11	AY037152 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AQ229478/c 466 bp DNA linear GSS 26-SEP-1998
DEFINITION HS.2021.A2.A08.MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2021 COL=16 Row=A, DNA sequence.
ACCESSION AQ229478
VERSION AQ229478.1 GI:3654707
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,D., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2021 row: A column: 16

Class: BAC ends
High quality sequence stop: 466.

FEATURES
Location/Qualifiers
1. 466

BASE COUNT 113 a 94 c 111 g 147 t 1 others
ORIGIN
Query Match 12.8%; Score 110.8; DB 17; Length 466;
Best Local Similarity 90.8%; Pred. No. 1.3e-18;
Matches 118; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGTACTCAGGAGCGTGAACGAGATCGCTGAACCCGAGAGGAGAGTTCAGTG 60
|||||
Db 399 AGTACTCAGGAGCGTGAACGAGATCGCTGAACCCGAGAGGAGTTCAGTG 340
QY 61 AGCCGAGATCAGCCGCTAGACTCCATCCAGCTGGCGGAAAGAGCAAGACTCCGTCTCA 120
|||||
Db 339 AGCCGAGATCAGCCGCTAGACTCCATCCAGCTGGCGGAAAGAGCAAGACTCCGTCTCA 280
QY 121 AAAAAAAAAA 130
|||||
Db 279 AAAAAAAAAA 270

RESULT 2
AG186502 680 bp DNA linear GSS 09-JAN-2002
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-060015.T7, genomic survey
ACCESSION AG186502
VERSION AG186502.1 GI:16716182
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
ORGANISM Male BAC library clone:RP43-060015.T7.

REFERENCE
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoh.Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 680)
TITLE Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoh.Y., Watanabe,H. and Sakaki,Y.
JOURNAL Direct Submission
AUTHORS Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenho-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpsesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the Rad process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7

LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 680
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-060015.T7"
/sex="male"

FEATURES
source

BASE COUNT 194 a 156 c 163 g 121 t 46 others
ORIGIN
Query Match 12.6%; Score 109.2; DB 17; Length 680;
Best Local Similarity 87.0%; Pred. No. 3.5e-18;
Matches 120; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGTACTCAGGAGCGTGAACGAGATCGCTGAACCCGAGAGGAGAGTTCAGTG 60
|||||
Db 239 AGTACTCAGGAGCGTGAACGAGATCGCTGAACCCGAGAGGAGTTCAGTG 298
QY 61 AGCCGAGATCAGCCGCTAGACTCCATCCAGCTGGCGGAAAGAGCAAGACTCCGTCTCA 120
|||||
Db 299 AGCCGAGATCAGCCGCTAGACTCCATCCAGCTGGCGGAAAGAGCAAGACTCCGTCTCA 358
QY 121 AAAAAAAAAA 138
|||||
Db 359 AAAAAAAAAA 376

RESULT 3
AQ390169 418 bp DNA linear GSS 06-MAR-1999
LOCUS
DEFINITION CITR1-El-2544A19.TF CITR1-El Homo sapiens genomic clone 2544A19,
DNA sequence.
ACCESSION AQ390169
VERSION AQ390169.1 GI:4361192
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
Zhaio,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: CITR1-El-2544A19.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
1. 418
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2544A19"
/clone_lib="CITR1-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library p"

BASE COUNT 132 a 109 c 104 g 73 t
ORIGIN
Query Match 12.4%; Score 107.6; DB 17; Length 418;
Best Local Similarity 86.2%; Pred. No. 8.9e-18;
Matches 119; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 AGTACTCAGGAGCGTGAACGAGATCGCTGAACCCGAGAGGAGAGTTCAGTG 60
|||||
Db 95 AGTACTCAGGAGCGTGAACGAGATCGCTGAACCCGAGAGGAGAGTTCAGTG 154

0y 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCCTGGCGGAAAGACAGACTCCCTCTCA 120
|||||
Db 155 AGCCGAGATCAGCCACTAGACTCCATCCAGCCCTGGCGGAAAGACAGACTCCCTCTCA 214
|||||
0y 121 AAAAAAAAAATCGTTTACA 138
|||||
Db 215 AAAAAAAAAAACAACA 232
|||||

RESULT 4
BM509394 469 bp mRNA linear EST 15-FEB-2002
LOCUS 1h7f10.y1 Human Insulinoma Homo sapiens cDNA 5' similar to
DEFINITION SW:ALU8.HUMAN P39195 ALU SUBFAMILY SX SEQUENCE CONTAMINATION
BM509394
ACCESSION BM509394.1 GI:18680537
VERSION EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 469)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scaerac,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R., Williams,T.,
Jackson,Y. and Bowers,Y.
, Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)
Seq primer: -40RP from G1bco
High quality sequence stop: 416.
Location/Qualifiers
FEATURES
Source
1. .469
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human Insulinoma"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site:2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer. In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda-protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 149 a 93 c 94 g 133 t
ORIGIN
Query Match 12.4%; Score 107.2; DB 13; Length 469;
Best Local Similarity 81.6%; Pred. No. 1.1e-17;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

0y 1 AGCTACTGAGGAGCTGACACAGAAATCGCTTGAACCCGGAGGACGAGCTTGCACTG 60
|||||

Db 285 AGCCACTGGGAGGCTTAAATGGAGAAATCGCTTGAACCCCTGGAGGACGAGCTTGCACTG 344
|||||
0y 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCCTGGCGGAAAGACAGACTCCCTCTCA 120
|||||
Db 345 AGCCGAGATCAGCCACTAGACTCCATCCAGCCCTGGCGGAAAGACAGACTCCCTCTCA 404
|||||
0y 121 AAAAAAAAAATCGTTTACAATTTATGTTGATT 152
|||||
Db 405 AAAAAAAAAAGTTAGAAAAATGCTCTTT 436
|||||

RESULT 5
B1468297 516 bp mRNA linear EST 11-MAR-2002
LOCUS i487b01.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE:5022649
DEFINITION 5', mRNA sequence.
B1468297
ACCESSION B1468297.1 GI:15284406
VERSION EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 516)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scaerac,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R., Williams,T.,
Jackson,Y. and Bowers,Y.
, Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)
High quality sequence stop: 457.
Location/Qualifiers
FEATURES
Source
1. .516
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5022649"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site:2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer. In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda-protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 157 a 103 c 104 g 152 t
ORIGIN
Query Match 12.4%; Score 107.2; DB 13; Length 516;
Best Local Similarity 81.6%; Pred. No. 1.2e-17;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

0y 1 AGCTACTGAGGAGCTGACACAGAAATCGCTTGAACCCGGAGGACGAGCTTGCACTG 60
|||||

Db 285 AGCCACTCGGAGGCTTAAATGGAGAAATCCGTTGAACCCCTGAGAGCAGAGCTTGCATGT 344

QY 61 AGCGAGATCAGCGACATCCATCCAGCTGGGGGAGGAAGACAGACTCCGTCTCA 120

Db 345 AGCCAGAGCCAGCGACATCCATCCAGCTGGGGTGGAGAGCAAGACTCATCTCA 404

QY 121 AAAAAAAAAATCGTTACATTTATGCTGATT 152

Db 405 AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

RESULT 6

LOCUS BQ270800 529 bp mRNA linear EST 07-MAY-2002

DEFINITION BQ270800.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE: 5779930

ACCESSION BQ270800

VERSION BQ270800.1 GI:20495866

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagaratshvili,R., Williams,T., Jackson,Y., and Bowers,Y.,

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Other ESTs: Jk05b06.x1

CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer In vivo mass-excised to pluscript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence stop: 428.

Location/Qualifiers

1. 529

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE: 5779930"

/clone_id="Human Insulinoma"

/tissue_type="Insulinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pBluescript SK-; Site:1: XhoI; Site:2: EcoRI; Constructed with lambda ZapIT system (Stratagene) by Dr. J. Ferrer. In vivo mass-excised to pluscript SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

BASE COUNT 160 a 107 c 107 g 155 t

ORIGIN

Query Match 12.4%; Score 107.2; DB 14; Length 529;

Best Local Similarity 81.6%; Pred. No. 1.2e-17;

Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 AGTACTCAGAGGCTGTGACACAGAAATCGTTGAACCCCGAGAGCAGAGCTGCATGT 60

Db 285 AGCCACTCGGAGGCTTAAATGGAGAAATCCGTTGAACCCCTGAGAGCAGAGCTTGCATGT 344

QY 61 AGCGAGATCAGCGACATCCATCCAGCTGGGGGAGGAAGACAGACTCCGTCTCA 120

Db 345 AGCCAGAGCCAGCGACATCCATCCAGCTGGGGTGGAGAGCAAGACTCATCTCA 404

QY 121 AAAAAAAAAATCGTTACATTTATGCTGATT 152

Db 405 AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

RESULT 7

LOCUS BQ267333 556 bp mRNA linear EST 07-MAY-2002

DEFINITION BQ267333.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE: 5779589

ACCESSION BQ267333

VERSION BQ267333.1 GI:20492398

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scaerac,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagaratshvili,R., Williams,T., Jackson,Y., and Bowers,Y.,

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer In vivo mass-excised to pluscript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence stop: 428.

Location/Qualifiers

1. 556

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE: 5779589"

/clone_id="Human Insulinoma"

/tissue_type="Insulinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pBluescript SK-; Site:1: XhoI; Site:2: EcoRI; Constructed with lambda ZapIT system (Stratagene) by Dr. J. Ferrer. In vivo mass-excised to pluscript SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

BASE COUNT 167 a 112 c 113 g 164 t

ORIGIN

Query Match 12.4%; Score 107.2; DB 14; Length 556;

Best Local Similarity 81.6%; Pred. No. 1.2e-17;

Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY	1	AGCTACTGAGAGCGTGAACAGAGAAATCGCTTGTAACCCGGAGCAGAGCTTCAGNG	60
Db	285	AGCCAGATCGGGAGCGTTAAATGAGGAATCGCTTAAACCCTTGAGAGCAGAGCTTCAGTG	344
OY	61	AGCCGAGATCAAGCCGCATAGATCCATCCAGCTGGGGAAAAGACAGACTCCGTCTCA	120
Db	345	AGCCAGACACAGCCACTGCATCCATCCAGCTGGTGAGAGACAGACTCATCTCA	404
OY	121	AAAAAAAAAATCGTTACAATTATGCTGGATT	152
Db	405	AAAAAAAAAAAAAGTTAGAAAAAATCTCTCTT	436
RESULT 8			
LOCUS	BQ270346	589 bp	mRNA linear EST 07-MAY-2002
DEFINITION	1K09g10.y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5780562		
ACCESSION	BQ270346		
VERSION	BQ270346.1	GI:20495412	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Eumetazoa; Eutheta; Primates; Carnivora; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 589)		
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kastner,K., Lemshka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blaisdell,A., Schmitt,A., Theising,B., Riltter,E., Ronko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y. Endocrine Pancreas Consortium Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@oebiohp.harvard.edu Library was constructed by Dr. J. Ferrer In vivo mass-excised to pluiscrypt SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@elm.wustl.edu) Seq primer: -40RP from Gbpco High quality sequence stop: 427. Location/Qualifiers 1..589 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE: 5780562" /clone_lib="Human Insulinoma" /cissue_type="Insulinoma" /lab_host="DH10B (phage-resistant)" /note="Organ: pancreas; Vector: pluiscrypt SK-. Site: 1: XhoI; Site: 2: EcoRI; Constructed with lambda ZAPI system (Stratagene) by Dr. J. Ferrer. In vivo mass-excised to pluiscrypt SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: This is a Washington University Pancreas EST project library."		
BASE COUNT	177 a	122 c	116 g 174 t
ORIGIN			
Query Match	12.4%	Score 107.2;	DB 14; Length 589;
Best Local Similarity	81.6%;	Pred. No. 1.2e-17;	

	Matches	124:	Conservative	0:	Mismatches	28:	Indels	0:	Gaps	0:
OY	1	AGCTACTCAGGAGCGTGGACACGAGATCCGTTAAACCCGGGAGGCAGAGTGTCAGTG	60							
Db	285	AGCCACTCGGGGCGTTAAATGGGGGAATCGCTTAAACCCTGGAGGACAGAGTTCGACTG	344							
OY	61	AGCCGAGATTCACGCCACTAGACTCATTCACGCTGGCGGGAAGAAGACAAGACTCCGTCA	120							
Db	345	AGCCAGGACCCACGCCACTGCACTCCATCCACTGAGCTGGGTGACAGACCAAGACTCCATCTCA	404							
OY	121	AAAAAAAAAATCGTTACAAATTTATGGTGAAATT	152							
Db	405	AAAAAAAAAAAAAGTTAGAAAATCTCTCTTT	436							
RESULT 9										
AQ428429			635 bp	DNA		linear	GSS 24-MAR-1999			
LOCUS										
DEFINITION	CITBI-EI-2564J3.TF CITBI-EI Homo sapiens genomic clone 2564J3, DNA sequence.									
ACCESSION	AQ428429									
VERSION	AQ428429.1									
KEYWORDS	GSS.									
SOURCE	human.									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
AUTHORS	1 (bases 1 to 635) Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.									
TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building									
JOURNAL	unpublished (1997)									
COMMENT	Other-GSS: CITBI-EI-2564J3.TF Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are available from Research Genetics (inforesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.									
FEATURES										
Source	location/qualifiers									
	1..635	/organism="Homo sapiens"								
	/db_xref="taxon:9606"									
	/clone="2564J3"									
	/clone_lib="CITBI-EI"									
	/sex="male"									
	/cell_type="sperm"									
	/note="Vector: pBeloBAC11, Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"									
BASE COUNT	218 a 129 c 119 g 169 t									
ORIGIN										
Query Match	12.3%.	Score 106.4;	DB 17;	Length 635;						
Best Local Similarity	67.3%.	Pred. No. 1.9e-17;								
Matches 167:	Conservative	0:	Mismatches	76;	Indels	5;	Gaps	1;		
OY	1	AGCTCTCAGGAGGGGTGAGACGAGAAATGCGTTGAACCCGGGAGGCAGAGTTCAGTG	60							
Db	307	AGCTATTAGAGACGCTTGAGGACGAGGAATCACTTGAACCCGGGAGGTGAGAGTTACAGTG	366							
OY	61	AGCCGAGATTCACGCCACTAGACTCATTCACGCTGGCGGGAAGAAGACAAGACTCCGTCA	120							
Db	367	AGCCGAGATTCGCGCACACGCACTCCATCCACTGAGCTGGCAGACAGATGAGACTCCAGCTCA	426							
OY	121	AAAAAAAAAATCGTTACAA-----TTATGGTGAAATTACTCCCTCTTTTAACCTCATCA	175							

Db	427	AAAAAAAAAAAAAAAAATTCACCTTTAAACGTGCTACCTACACCCAGCTTGATCGACAA	486
QY	176	AGACACAGCAGCTACTTTAAAGCAAGTCATGATTTGAACGCCCTTTCTTTCCATAATAA	235
Db	487	ACTACACAGAGCTATAGATTAACCTTATTTATGATTTACACAGATTTATTTGATATAATA	546
QY	236	GGGAGATT 243	
Db	547	TAGACAGT 554	
RESULT 10			
AQ751486			
LOCUS			
DEFINITION	AQ751486	774 bp	DNA
LOCUS	HS-5576_B2-B05.SP6 RPCI-11 Human Male BAC Library Homo sapiens		linear GSS 19-JUL-1999
ACCESSION	AQ751486		
VERSION	AQ751486.1		
KEYWORDS	GSS.	GI:5538644	
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 774)		
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,		
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and		
	Hood L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and		
	scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	96 (17),	9739-9744 (1999)
MEDLINE	99380589		
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L		

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel.: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPc1-11. For BAC library availability, please contact Pieter de Jong (pieter@ejonq.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (Info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 1152 row: D column: 10
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 774.

FEATURES	source	Location/Qualifiers
	1. .774	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="Plate1152 Col=10 Row=D" /clone_id="RPC1-11 Human Male BAC library" /sex="male"
		/note="Vector: pBAC3.6; Site.1: EcoRI; Site.2: EcoRI; Male blood DNA was isolated from a randomly chosen donor and partially digested with a combination of EcoRI and EcoRII. Methyase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
BASE COUNT	258 a	192 c 177 g 143 t 4 others
BRGIN		

Query Match	12.2%	Score 106;	DB 17;	Length 774;
Best Local Similarity	88.5%	Pred. No. 2.5e-17;		
Matches 115; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

QY	1	AGCTACTAGAGAGGCTGAGACACAGAAATCCGCTTGAACCCGGGAGGCGAGAGTTGCACTG	60
Db	248	AGCTATCTGAGAGGCTGAGCGAGAGAAATGCGATGAACCTGGGAGATGCGAGACTTGGCACTG	307
OY	61	AGCCGAGATCAGCGCCACTAGACTGCATCCAGCTTGGCGGAAGAAGCAAGACTCCGCTCTCA	120

Db	QY	Db
308	121	368
AGCCAGATCTCGCCACTGCATCCTCCATCCAGCCCTGGGGGACAGAGCGAGACTGTCTCA	AAAAAAAA 130	AAAAAAAAAA 377

RESULT 11	
LOCUS	671 bp
DEFINITION	DNA
	1 linear
	GSS 23-MAR-1999
	RPCL1-11-179H11.TV
	RPCL1-11-179H11
	Homo sapiens genomic clone RPCL1-11-179H11
	/ DNA sequence.

ACCESSION	AA018931	
VERSION	AA018931.1	GI:4476655
KEYWORDS	GS.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 671)

Zhao, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and Venter, J.C.

TITLE	Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready Map Building
JOURNAL	unpublished (1997)
COMMENT	Other_GSSS: RPCT-11-179H11.TU

Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org
Clones are derived from the human BAC library RPCR-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.ligr.org/ldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES	SOURCE
Location/Qualifiers	1..671
/organism="Homo sapiens"	
/db_xref="GDB:7568530"	
/db_xref="taxon:9606"	
/clone="RPC1-11-179H11"	
/clone_1id="RPC1-11"	
/sex="Male"	
/cell_type="Lymphocytes"	
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC library"	
BASE COUNT	237 a 166 c 155 g 113 t
ORIGIN	

Query Match	12.1%	Score 104.8;	DB 17;	Length 671;
Best Local Similarity	84.3%	Pred No. 5.1e-17;		
Matches 118; Conservative	0;	Mismatches 22;	Indels 0;	Gaps 0;

OY 1 AGCTACTCAGAGAGCTGAGACACGAGAAATCGCTTGAAACCCGGGAGGACAGAGGTTGCAATG 60
 248 AGCTACTTCAAGAGGCTGAGAGGTGAGAAATGCGATGAATCTGGGATCTGAGAGCTTTGGACTG 307

61 AGCGGAGATCACGGCACTAGACTCCATCCACGCGTGGCGGAAGAAGCAGAAGACTCCGTCTCA 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
308 AGCGAAGATTCTGGCCACTGCACCTCATTCACGCTGGGGGCAAGAGCGAGATCTGTTCTCA 367

QY	121	AAAAAAATCGTTACAT	140
db	368	AAAAAAATCGTTACAT	387

RESULT 12

A0527107 465 bp DNA linear GSS 18-MAY-1999
LOCUS CITBI-EI-2603D20.TR CITBI-EI Homo sapiens genomic clone 2603D20,
DEFINITION DNA sequence.
ACCESSION A0527107.1 GI:4838867
VERSION A0527107.1
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 465)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hoeftlgr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source 1. .465
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2603D20"
/clone_lib="CITBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 157 a 102 c 109 g 97 t
ORIGIN
Query Match 12.1%; Score 104.6; DB 17; Length 465;
Best Local Similarity 78.6%; Pred. No. 5.6e-17;
Matches 125; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
OY 1 AGCTACTGAGAGGCTGAGACACGAGAAATCGCTGACCCGGAGGACAGAGTTCAGTG 60
|||||
DB 276 AGCTACTGAGAGGCTGAGAGGAGAAATCGCTGACCCGGAGGACAGAGTTCAGTG 335
OY 61 AGCCGAGATCACCGCAGTACATCCAGCTGGGGGAAAGACGACGATCCGCTCA 120
|||||
DB 336 AGTTAGATCACACACGCTACTCACTCCAGGCTGTGTGACGAGATGACATCTCC 395
OY 121 AAAAAAAAAAATCGTACAAATTTATGCTGGATCTACCC 159
|||||
DB 396 AAAAAAAAAAATTAATGATATACCTAACC 434
RESULT 13
LOCUS B0429052 815 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7908333 NIH_MGC_82 Homo sapiens CDNA clone IMAGE:6102430
5', mRNA sequence.
ACCESSION B0429052
VERSION B0429052.1 GI:21168128
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 815)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LICM237 row: a column: 23
High quality sequence stop: 479.
FEATURES
source 1. .815
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6102430"
/clone_lib="NIH_MGC_82"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggccatattgccc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATTTATGCGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCCGAGCGCCGACATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
BASE COUNT 241 a 188 c 178 g 208 t
ORIGIN
Query Match 12.1%; Score 104.6; DB 14; Length 815;
Best Local Similarity 83.2%; Pred. No. 5.9e-17;
Matches 119; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
OY 1 AGCTACTGAGAGGCTGAGACACGAGAAATCGCTTAACCCGGAGGACAGAGTTCAGTG 60
|||||
DB 163 AGCTACTGGGGGGCTGAGGACGAGGAATCGCTTAACCCGGAGGAGAGTTCAGTG 222
OY 61 AGCCGAGATCACCGCAGTACATCCAGCTGGGGGAAAGACGACGATCCGCTCA 120
|||||
DB 223 AGCCAAAGCTGGCGCAGTACCTCCAGCCTGGGGGACGACGACGACGACTCCGCTCG 282
OY 121 AAAAAAAAAAATCGTACAAATTTA 143
|||||
DB 283 AAAAAAAAAAATTAATGATATACCTAACC 305
RESULT 14
LOCUS BM672404/c 303 bp mRNA linear EST 27-FEB-2002
DEFINITION BM672404
UI-E-C00-adm-b-04-0-UI.s1 UI-E-C00 Homo sapiens CDNA clone
UI-E-C00-adm-b-04-0-UI 3', mRNA sequence.
ACCESSION BM672404
VERSION BM672404.1 GI:18982302
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 303)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250

Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 The following repetitive elements were found in this CDNA
 sequence: 11-303, >ALU (matched complement)
 Seq primer: M13 forward
 POLYA=yes

FEATURES

source 1. 303
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-C00-adm-b-04-0-UI"
 /clone_lib="UI-E-C00"
 /tissue_type="optic nerve"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-C00 is a CDNA library containing the following
 tissue(s): optic nerve. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT773-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (drl)8 tail. The
 sequence tag for this library is CCAATTAGTG. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI).
 TAG_LTB=UI-E-C00
 TAG_TISSUE=human
 TAG_SEQ=CCATTAGTG"
 BASE COUNT 51 a 97 c 74 g 81 t
 ORIGIN

Query Match 12.0%; Score 104.4; DB 14; Length 303;
 Best Local Similarity 87.7%; Pred. No. 6e-17;
 Matches 114; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACAGAGATCGCTTGAACCCGGAGGAGAGGTTGCAGTG 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 137 AGCTGCTCGGAGGCTGAGGAGAGATGCGTGAACCCGAGGAGAGAGCTTGCAGTG 78
 QY 61 AGCGAGATCAGCGCACTAGACTCATCCAGCCTGGGCGAAGAGCAAGACTCGGTCTCA 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 77 AGCGAGATTCGCGCACTGCACTCATCCGCGCTGGGTGACAGAGCAAGACTCGGTCTA 18
 QY 121 AAAAAAAAAA 130
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 17 AAAAAAAAAA 8

RESULT 15
 AG139751 712 bp DNA linear GSS 04-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-154F08.F, genomic survey sequence.
 DEFINITION AG139751
 ACCESSION AG139751
 VERSION AG139751.1 GI:16669429
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
 BAC library clone:PTB-154F08.F.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.
 BAC end sequences of Library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 712)
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the Rad process and may have higher chance of
 clone tracking errors.

COMMENT

PRIMERS
 Sequencing: -21M13
 LIBRARY
 Vector : PKS145
 R.Site 1 : SacI
 R.Site 2 : SacI
 Location/Qualifiers
 1. 712
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-154F08.F"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"
 BASE COUNT 159 a 166 c 143 g 243 t
 ORIGIN

Query Match 12.0%; Score 104.4; DB 17; Length 712;
 Best Local Similarity 87.7%; Pred. No. 6.e-17;
 Matches 114; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACAGAGATCGCTTGAACCCGGAGGAGAGGTTGCAGTG 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 340 AGCTACTCCGGAGGCTGAGGAGAGATCGCTTGAACCAAGAGGAGAGGTTGCAGTG 281
 QY 61 AGCGAGATCAGCGCACTAGACTCATCCAGCCTGGGCGAAGAGCAAGACTCGGTCTCA 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 280 ACCGAGATCGCGCACTGCACTCATCCAGCCTGGGCGAGAGAGTGAAGTATGTCTCA 221
 QY 121 AAAAAAAAAA 130
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 220 AAAAAAAAAA 211

Search completed: January 25, 2003, 16:30:57
 Job time : 2260 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:39:25 : Search time 76 seconds
(without alignments)
3498.536 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867
1 agctactcagagagctcgtaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/prodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/prodata/2/1na/5A_COMB.seq:*
4: /cgn2_6/prodata/2/1na/5B_COMB.seq:*
5: /cgn2_6/prodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/1na/backfillsl.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	848.6	97.9	2420	1	US-08-330-123A-3	Sequence 3, Appl1
2	848.6	97.9	2420	4	US-09-380-517-3	Sequence 3, Appl1
3	848.6	97.9	2426	1	US-08-482-115B-3	Sequence 3, Appl1
4	848.6	97.9	2426	2	US-08-660-678A-3	Sequence 3, Appl1
5	848.6	97.9	2426	2	US-08-472-802C-4	Sequence 4, Appl1
6	848.6	97.9	2426	2	US-08-714-482-1	Sequence 1, Appl1
7	848.6	97.9	2426	3	US-08-998-443-3	Sequence 3, Appl1
8	848.6	97.9	2426	4	US-09-060-523-3	Sequence 3, Appl1
9	834.6	96.3	2425	2	US-08-485-778-1	Sequence 1, Appl1
10	834.6	96.3	2425	3	US-08-520-550A-1	Sequence 1, Appl1
11	334	38.5	981	2	US-08-710-482-5	Sequence 2, Appl1
12	333	38.4	981	2	US-09-220-157A-5	Sequence 5, Appl1
13	333	38.4	981	4	US-09-349-532-22	Sequence 22, Appl1
14	332.4	38.3	981	2	US-08-833-377-1	Sequence 1, Appl1
15	332.4	38.3	981	2	US-08-838-545-22	Sequence 22, Appl1
16	332.4	38.3	981	4	US-09-349-532-22	Sequence 22, Appl1
17	332.4	38.3	981	4	US-09-851-896-3	Sequence 22, Appl1
18	99.4	11.5	70000	4	US-08-324-465-2	Sequence 2, Appl1
19	97.6	11.3	1656	2	US-08-465-981-2	Sequence 2, Appl1
20	97.6	11.3	1656	5	PCT-US93-11915-2	Sequence 2, Appl1
21	97.6	11.3	1725	1	US-08-324-465-5	Sequence 5, Appl1
22	97.6	11.3	1725	2	US-08-465-981-5	Sequence 5, Appl1
23	97.6	11.3	1725	5	PCT-US93-11915-5	Sequence 5, Appl1
24	97.4	11.2	11811	4	US-09-078-294-7	Sequence 7, Appl1
25	97.4	11.1	1701	4	US-09-078-294-9	Sequence 9, Appl1
26	96.4	11.1	99500	4	US-09-798-096-10	Sequence 10, Appl1
27	96	11.1	99500	4	US-09-798-096-10	Sequence 10, Appl1

C	28	95.6	11.0	14636	4	US-09-173-914-6	Sequence 6, Appl1
C	29	95.4	11.0	36159	4	US-09-749-588-3	Sequence 3, Appl1
C	30	95	11.0	9837	1	US-08-832-883-68	Sequence 68, Appl1
C	31	95	11.0	9837	2	US-08-832-877-68	Sequence 68, Appl1
C	32	94.8	10.9	176373	3	US-09-128-155-17	Sequence 17, Appl1
C	33	94.4	10.9	955	4	US-09-641-638-4	Sequence 4, Appl1
C	34	94.4	10.9	955	4	US-09-641-638-5	Sequence 5, Appl1
C	35	94.4	10.9	955	4	US-09-641-638-6	Sequence 6, Appl1
C	36	94.4	10.9	955	4	US-09-641-638-7	Sequence 7, Appl1
C	37	94.4	10.9	1000	4	US-09-641-638-650	Sequence 650, Appl1
C	38	94.4	10.9	3609	4	US-09-705-299-11	Sequence 11, Appl1
C	39	94.4	10.9	3844	4	US-09-689-423-1	Sequence 1, Appl1
C	40	94.4	10.9	246240	2	US-08-724-394A-20	Sequence 20, Appl1
C	41	94.4	10.9	246240	2	US-08-724-394A-21	Sequence 21, Appl1
C	42	94.4	10.9	246240	2	US-08-724-394A-22	Sequence 22, Appl1
C	43	94	10.8	866	4	US-09-257-179-11	Sequence 11, Appl1
C	44	94	10.8	2387	4	US-09-375-318-38	Sequence 38, Appl1
C	45	94	10.8	112132	4	US-09-741-150-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-330-123A-3
; Sequence 3, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTREAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; City: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-330-123A-3
Query Match 97.9%; Score 848.6; DB 1; Length 2420;
Best Local Similarity 99.4%; Pred. No. 1.2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Oy	1	AGTACTCAGSAGGCTGAGACAGCAGAAATGCGTTGAAACCCGGAGGCGAGAGGTTCCAGTG	60
Db	662	AGCTACTCAGGAGGCTGAGACAGAGAAATGCGTTGAAACCCGGGA-6CAGAGGTTCCAGTG	720
Oy	61	AGCCGAGATCAGGCGACCTAACACTCCAGCGCTGGGGCGAAAGACAAACTCCGTCGA	120
Db	721	AGCCGAGATCAGGCGACCTAACACTCCAGCGCTGGGGCGAAAGACAAACTCCGTCGA	780
Oy	121	AAAAAAAAATCGTTACAAATTTATGGTGATTTACTCCCTCTTTTATCCTCATCAAGACA	180
Db	781	AAAAAAAAAAATCGTTACAAATTTATGGTGATTTACTCCCTCTTTTATCCTCATCAAGACA	840
Oy	181	CAGCACTACTTTAAAGCAAAAGTCAAATGATTAAGCAAGCGCTTCTTCTCTATATAAGGAG	240
Db	841	CAGCACTACTTTAAAGCAAAAGTCAAATGATTAAGCAAGCGCTTCTTCTCTATATAAGGAG	900
Oy	241	ATTGAGTCTTTAAGATTAATATATGATAGTATACACTTGATTAAGAGCCATCCCTGTCGA	300
Db	901	ATTGAGTCTTTAAGATTAATATATGATAGTATACACTTGATTAAGAGCCATCCCTGTCGA	960
Oy	301	AGGGAAGCTGGAGAACGCAATTCCTAAAGAAAAAGGGGCAAGGCTTGGAACTCGGAGCCATC	360
Db	961	AGGGAAGCTGGAGAACGCAATTCCTAAAGAAAAAGGGGCAAGGCTTGGAACTCGGAGCCATC	1020
Oy	361	CCACTGAGCCGAGACAAGATTTGCTGTAGTCAGTCTCCTCGGGAAATCTATTTCACAA	420
Db	1021	CCACTGAGCCGAGACAAGATTTGCTGTAGTCAGTCTCCTCGGGAAATCTATTTCACAA	1080
Oy	421	AGTTCTCCAAAAATGATGATCAAAACCTAGCAATTAATGTTTCTGTGCTTAGGCGCTTA	480
Db	1081	AGTTCTCCAAAAATGATGATCAAAACCTAGCAATTAATGTTTCTGTGCTTAGGCGCGCTTA	1140
Oy	481	AAATCTTCTGTGAATTCATATTTTAAAGTAGTCGAGTAGGAACCGGCTGGTGTGCGAGA	540
Db	1141	AAATCTTCTGTGAATTCATATTTTAAAGTAGTCGAGTAGGAACCGGCTGGTGTGCGAGA	1200
Oy	541	GGATAGAAAAAGGCGCTCTGATTAAGCTCAAGTTAGTTTACCTTTAAAGAAAGTCGAGAC	600
Db	1201	GGATAGAAAAAGGCGCTCTGATTAAGCTCAAGTTAGTTTACCTTTAAAGAAAGTCGAGAC	1260
Oy	601	TAAAGACGCAAAAGCTTTCCCGGAGCTGGGGAAAGGGCAACGTCCTTCCATAGGCGCGAA	660
Db	1261	TAAAGACGCAAAAGCTTTCCCGGAGCTGGGGAAAGGGCAACGTCCTTCCATAGGCGCGAA	1320
Oy	661	ATGGAACCTTAATTTCCCGTTCCCGCCCAACCAAGCCCGCCCGAGAGAGTAGCTCTACAGAG	720
Db	1321	ATGGAACCTTAATTTCCCGTTCCCGCCCAACCAAGCCCGCCCGAGAGAGTAGCTCTACAGAG	1380
Oy	721	AGCCGAGAGTCAAGCTTGGGCCAATCCGTCGGGTGGGGGCGCTCCCTTTATAAGCCGA	780
Db	1381	AGCCGAGAGTCAAGCTTGGGCCAATCCGTCGGGTGGGGGCGCTCCCTTTATAAGCCGA	1440
Oy	781	CTCGCCCGGAGCGCACCGGGTTGCGAGAGGTGGGCTTGGAGGGGTGGTGGCCATTTT	840
Db	1441	CTCGCCCGGAGCGCACCGGGTTGCGAGAGGTGGGCTTGGAGGGGTGGTGGCCATTTT	1500
Oy	841	TGCTTAACCTTAAGTAGAAGGGCGTTA	867
Db	1501	TGCTTAACCTTAAGTAGAAGGGCGTTA	1527

RESULT 2
US-09-580-517-3
Sequence 3, Application US/09580517
Patent No. 6320039
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
FENG, Junli
FUNK, Walter
ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

```

1 ADDRESS: Townsend and Townsend Kourie and Crew
2
3 STREET: 379 Lytton Avenue
4
5 CITY: Palo Alto
6
7 STATE: California
8
9 COUNTRY: US
10
11 ZIP: 94301
12
13 COMPUTER READABLE FORM:
14
15 MEDIUM TYPE: floppy disk
16
17 COMPUTER: IBM PC compatible
18
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20
21 SOFTWARE: patentin Release #1.0, Version #1.25
22
23 CURRENT APPLICATION DATA:
24
25 APPLICATION NUMBER: US/09/580,517
26
27 FILING DATE: 25-May-2000
28
29 CLASSIFICATION: <Unknown>
30
31 PRIOR APPLICATION DATA:
32
33 APPLICATION NUMBER: 08/330,123
34
35 FILING DATE: <Unknown>
36
37 ATTORNEY/AGENT INFORMATION:
38
39 NAME: Smith, William M
40
41 REGISTRATION NUMBER: 30,223
42
43 REFERENCE/DOCKET NUMBER: 15389-000810
44
45 TELECOMMUNICATION INFORMATION:
46
47 TELEPHONE: (415) 326-2400
48
49 TELEFAX: (415) 326-2422
50
51 INFORMATION FOR SEQ ID NO: 3:
52
53 SEQUENCE CHARACTERISTICS:
54
55 LENGTH: 2420 base pairs
56
57 TYPE: nucleic acid
58
59 STRANDEDNESS: single
60
61 TOPOLOGY: linear
62
63 MOLECULE TYPE: DNA (genomic)
64
65 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
66
67 US-09-580-517-3

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Query Match	97.9%	Score 848.6;	DB 4;	Length 2420;
Best Local Similarity	99.4%	Pred. No. 1.2e-263;		
Matches 862;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;
QY 1	AGCTACTCAGCAGGCTGTGAGACAGAGAAATCCCTTGAACCCGGAGGCGAGAGTGGCAGTG	60		
Db 662	AGCTACTGTGAGGCTGTGAGACAGAGAAATCCCTTGAACCCGGAGGCGAGAGTGGCAGTG	720		
QY 61	AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGGGGAAGAGCAAGACTCCGTCTCA	120		
Db 721	AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGGGGAAGAGCAAGACTCCGTCTCA	780		
QY 121	AAAAAAAAAAATCGTTACATTTATGGGGATTACTCCGCCCTTTTAACTCATCAATAACAA	180		
Db 781	AAAAAAAAAAATCGTTACATTTATGGGGATTACTCCGCCCTTTTAACTCATCAATAACAA	840		
QY 181	CAGCACTACTTTAAAGCAAGCAATGTAAGAAAGCGCTTTCTTTCTCTAATAAAGGAG	240		
Db 841	CAGCACTACTTTAAAGCAAGCAATGTAAGAAAGCGCTTTCTTTCTCTAATAAAGGAG	900		
QY 241	ATTGAGTCCTTAAGATTAATAATGTAGTATGTTAACTTGATTTAAAGCCATTCCTGCTCA	300		
Db 901	ATTGAGTCCTTAAGATTAATAATGTAGTATGTTAACTTGATTTAAAGCCATTCCTGCTCA	960		
QY 301	AGGAGAAGCTGGAGAAGGCATTTCTAAGGAAAAAAGGGGACAGGCTGGAAATCGACGCATC	360		
Db 961	AGGAGAAGCTGGAGAAGGCATTTCTAAGGAAAAAAGGGGACAGGCTGGAAATCGACGCATC	1020		
QY 361	CCACTGAGCCGACAGCAAGATTTCTGCTGTAGTCACTGCTGCCCTGGGAATCTAATTTTCAAA	420		
Db 1021	CCACTGAGCCGACAGCAAGATTTCTGCTGTAGTCACTGCTGCCCTGGGAATCTAATTTTCAAA	1080		
QY 421	AGTTCTCCAAAAAATGTGATGATCAAAACTAGAAATTAAGTTCTGTGCTTTAGGGCCCTA	480		
Db 1081	AGTTCTCCAAAAAATGTGATGATCAAAACTAGAAATTAAGTTCTGTGCTTTAGGGCCCTA	1140		
QY 481	AAATCTTCTGTGATTCCAATTTTAAAGTAGTGTGAGGTGAACCGCTGTGCTTGCGACA	540		

Db 1141 AATCTTCTGTGAATTCATTTTAAAGTAGTCGAGTGCAACCGCTGTCTCCAGA 1200
OY 541 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTGGGAAG 600
Db 1201 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTGGGAAG 1260
OY 601 TAAAGACGAACGCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTATGGCCGGA 660
Db 1261 TAAAGACGAACGCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTATGGCCGGA 1320
OY 661 ATGGAATTTAATTTCCCGTTCCTCCCAACACGACCCCGGAGAGTAGTCTCACGAG 720
Db 1321 ATGGAATTTAATTTCCCGTTCCTCCCAACACGACCCCGGAGAGTAGTCTCACGAG 1380
OY 721 AGCGGAGAGTAGTCTGAGCAATCGTGCAGGTCGCGGCGGCTCCCTTATTAAGCCGA 780
Db 1381 AGCGGAGAGTAGTCTGAGCAATCGTGCAGGTCGCGGCGGCTCCCTTATTAAGCCGA 1440
OY 781 CTCGCCCCGAGCGACACCGGTTGCGAGAGGTGGGCTGGAGGGGTGTCGCAATTTT 840
Db 1441 CTCGCCCCGAGCGACACCGGTTGCGAGAGGTGGGCTGGAGGGGTGTCGCAATTTT 1500
OY 841 TGTCTAACCTTAAGTGAAGAGGCGTA 867
Db 1501 TGTCTAACCTTAAGTGAAGAGGCGTA 1527

RESULT 3
US-08-482-115B-3
; Sequence 3, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Assays for the RNA Component of Human
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00083005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-482-115B-3
Query Match 97.9%; Score 848.6; DB 1; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 AGCTACTCAGAGAGGCTGAGACACAGAGAAATCGCTTGAACCCGGGAGGACAGAGTTGACAGTG 60
Db 662 AGCTACTCAGAGAGGCTGAGACACAGAGAAATCGCTTGAACCCGGGAG-CCAGAGGTTGAGTG 720
OY 61 AGCGGAGATCACCCCTAGACTCCTCATCCAGCTGAGGCGGAAGAAGACAGCTCCGCTCA 120
Db 721 AGCGGAGATCACCCCTAGACTCCTCATCCAGCTGAGGCGGAAGAAGACAGCTCCGCTCA 780
OY 121 AAAAAAAAAATCTTCAATTTATGTTGATTAATCTCCCTCTTTTAACTCATCAAGACA 180
Db 781 AAAAAAAAAATCTTCAATTTATGTTGATTAATCTCCCTCTTTTAACTCATCAAGACA 840
OY 181 CAGCACTACTTTAAAGCAAGTCAATGATTGAAGCGCTTTCTTCTCTAATAAAGGAG 240
Db 841 CAGCACTACTTTAAAGCAAGTCAATGATTGAAGCGCTTTCTTCTCTAATAAAGGAG 900
OY 241 ATTCAGTCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 901 ATTCAGTCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
OY 301 AGGAGAGCTGAGAGAGGCAATCTTAAGGAAAAAGGGGCAAGGTTGGACATCGAGCAGATC 360
Db 961 AGGAGAGCTGAGAGAGGCAATCTTAAGGAAAAAGGGGCAAGGTTGGACATCGAGCAGATC 1020
OY 361 CCACAGAGCGGAGACAAAGATTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 420
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OY 421 AGTTTCGCAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 1081 AGTTTCGCAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
OY 481 AATCTTCTGTGAATTCATTTTAAAGTAGTCGAGTGCAACCGGCTGTCTCCAGA 540
Db 1141 AATCTTCTGTGAATTCATTTTAAAGTAGTCGAGTGCAACCGGCTGTCTCCAGA 1200
OY 541 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTGGGAAG 600
Db 1201 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTGGGAAG 1260
OY 601 TAAAGACGAACGCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTATGGCCGGA 660
Db 1261 TAAAGACGAACGCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTATGGCCGGA 1320
OY 661 ATGGAATTTAATTTCCCGTTCCTCCCAACACGACCCCGGAGAGTAGTCTCACGAG 720
Db 1321 ATGGAATTTAATTTCCCGTTCCTCCCAACACGACCCCGGAGAGTAGTCTCACGAG 1380
OY 721 AGCGGAGAGTAGTCTGAGCAATCGTGCAGGTCGCGGCGGCTCCCTTATTAAGCCGA 780
Db 1381 AGCGGAGAGTAGTCTGAGCAATCGTGCAGGTCGCGGCGGCTCCCTTATTAAGCCGA 1440
OY 781 CTCGCCCCGAGCGACACCGGTTGCGAGAGGTGGGCTGGAGGGGTGTCGCAATTTT 840
Db 1441 CTCGCCCCGAGCGACACCGGTTGCGAGAGGTGGGCTGGAGGGGTGTCGCAATTTT 1500
OY 841 TGTCTAACCTTAAGTGAAGAGGCGTA 867
Db 1501 TGTCTAACCTTAAGTGAAGAGGCGTA 1527

RESULT 4
US-08-660-678A-3
; Sequence 3, Application US/08660678A
; Patent No. 5837857

GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-660-678A-3

Query Match 97.9%; Score 848.6; DB 2; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTCAGGAGGCTGAGACACGAGANTCGTTGAACCCGGGAGCGAGGTTGCAGTG 60
DB 662 AGCTACTCAGGAGGCTGAGACACGAGANTCGTTGAACCCGGGAGCGAGGTTGCAGTG 720
QY 61 AGCCGAGATCAGCCGCTGAGCTCCATCCAGCCTGGCGGAAAGAGAGAGCTCCGCTCA 120
DB 721 AGCCGAGATCAGCCGCTGAGCTCCATCCAGCCTGGCGGAAAGAGAGAGCTCCGCTCA 780
QY 121 AAAAAAAAAATCTTACATTTATGTTGATTTACTCCCTCTTTTAAACCATCAAGACA 180
DB 781 AAAAAAAAAATCTTACATTTATGTTGATTTACTCCCTCTTTTAAACCATCAAGACA 840
QY 181 CAGCACTACTTTAAGCAAAAGTCATGATTGAAGCCCTTTCTTCTAATAAAGGAG 240
DB 841 CAGCACTACTTTAAGCAAAAGTCATGATTGAAGCCCTTTCTTCTAATAAAGGAG 900
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QY 301 AGGAGAGCTGAGAGCAATTTCTAAGCAAAAGGCGAGGTTGAGACGCGAGCATC 360
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QY 361 CCACTGAGCCGAGACAAAGATTCTGTAGTACGTGCTGCTGGAAATCATTTTCACA 420
DB 1021 CCACTGAGCCGAGACAAAGATTCTGTAGTACGTGCTGCTGCTGGAAATCATTTTCACA 1080
QY 421 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTAAGTTGTGTTAGGCCCTA 480
DB 1081 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTAAGTTGTGTTAGGCCCTA 1140
QY 481 AATCTCTCCGTAATTTCCATTTTAAAGTACGAGCGTGAACCCGCTGCTGCTCA 540
DB 1141 AATCTCTCCGTAATTTCCATTTTAAAGTACGAGCGTGAACCCGCTGCTGCTCA 1200
QY 541 GGATAGAAAAAGCCCTGTGATACCTCAAGTTACCTTTAAAGAGTGGAG 600
DB 1201 GGATAGAAAAAGCCCTGTGATACCTCAAGTTACCTTTAAAGAGTGGAG 1260
QY 601 TAAAGACCAAGCCCTTCCCGGAGCTGGGAGGCAACGTCCTTCATGCGCGAA 660
DB 1261 TAAAGACCAAGCCCTTCCCGGAGCTGGGAGGCAACGTCCTTCATGCGCGAA 1320
QY 661 ATGGAATTTAATTTCCGTTCCCGCCCAACGAGCCCGCGAGAGTGAATCTGACGAG 720
DB 1321 ATGGAATTTAATTTCCGTTCCCGCCCAACGAGCCCGCGAGAGTGAATCTGACGAG 1380
QY 721 AGCCGAGAGTCAAGCTTGAGCAATCCGTGCGGTCGCGCGCTCTTTAAGCCGA 780
DB 1381 AGCCGAGAGTCAAGCTTGAGCAATCCGTGCGGTCGCGCGCTCTTTAAGCCGA 1440
QY 781 CTGCGCCGCGAGCGCACCGGTTGCGGAGGTTGGCTTGGAGGGTGGCCATTTT 840
DB 1441 CTGCGCCGCGAGCGCACCGGTTGCGGAGGTTGGCTTGGAGGGTGGCCATTTT 1500
QY 841 TGCTAACCTTAAGTGAAGGCGCTA 867
DB 1501 TGCTAACCTTAAGTGAAGGCGCTA 1527

RESULT 5
US-08-472-802C-4
Sequence 4, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820

Db 662 AGTACTCAGGAGGCTGAGACAGCAAGTCCGTTGAACCCGGGA-GCAGAGTGTGCAATG 720
QY 61 AGCCGAGATCAGCGCAGTACAGCTCCATCCACCGTGGGGAAGCAAGACTCCGTCGA 120
Db 721 AGCCGAGATCAGCGCAGTACAGCTCCATCCACCGTGGGGAAGCAAGACTCCGTCGA 780
QY 121 AAAAAAAAAATGTTACAAATTTATGTGGATTACTCCCTCTTTTACCCTCATCAAGACA 180
Db 781 AAAAAAAAAATGTTACAAATTTATGTGGATTACTCCCTCTTTTACCCTCATCAAGACA 840
QY 181 CAGACACTCTTTAAAGCAAGTCAATGTTAAAGCGCTTTCTTCTTAATAAAGGAG 240
Db 841 CAGACACTCTTTAAAGCAAGTCAATGTTAAAGCGCTTTCTTCTTAATAAAGGAG 900
QY 241 ATTGAGTCCCTTAAGATTAATTAATGAGTGTACCTTGATTAAGCATCCCTGCTCA 300
Db 901 ATTGAGTCCCTTAAGATTAATTAATGAGTGTACCTTGATTAAGCATCCCTGCTCA 960
QY 301 AGGAGAGCTGGAGAGGCAATTTCTAAGGAAAAAGGGGAGGTTGAACTCGAGCGCATC 360
Db 961 AGGAGAGCTGGAGAGGCAATTTCTAAGGAAAAAGGGGAGGTTGAACTCGAGCGCATC 1020
QY 361 CCATGAGCCGAGACAGATTTCTCTAGTCACTGCTGCTGGGAATCTAATTTTCAAA 420
Db 1021 CCATGAGCCGAGACAGATTTCTCTAGTCACTGCTGCTGGGAATCTAATTTTCAAA 1080
QY 421 AGTCTCCAAAAATGTGATGATCAAAAGTAATAGTGTGCTGTGCTTAGGCCCTA 480
Db 1081 AGTCTCCAAAAATGTGATGATCAAAAGTAATAGTGTGCTGTGCTTAGGCCCTA 1140
QY 481 AATCTCTCTGTGATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGCTGTGAGA 540
Db 1141 AATCTCTCTGTGATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGCTGTGAGA 1200
QY 541 GGATAGAAAAAGGCGCTGATPACCTCAAGTGTGCTTCACTTTAAAGAGGTGCGAAG 600
Db 1201 GGATAGAAAAAGGCGCTGATPACCTCAAGTGTGCTTCACTTTAAAGAGGTGCGAAG 1260
QY 601 TAAAGACGCAAGGCTTTCCCGACGTGCGAGGCGCAAGCGCTCTCATGAGCGGAA 660
Db 1261 TAAAGACGCAAGGCTTTCCCGACGTGCGAGGCGCAAGCGCTCTCATGAGCGGAA 1320
QY 661 ATGGAATTTAATTTCCCGTTCGCCCAACAGCGCGCGGAGAGAGTGACTGTACAGAG 720
Db 1321 ATGGAATTTAATTTCCCGTTCGCCCAACAGCGCGCGGAGAGAGTGACTGTACAGAG 1380
QY 721 AGCGGAGAGTGAAGTGTGCGCAATCGGTGCGGCGCGCGCTCCCTTTATAAGCCGA 780
Db 1381 AGCGGAGAGTGAAGTGTGCGCAATCGGTGCGGCGCGCGCTCCCTTTATAAGCCGA 1440
QY 781 CTCGCCCGGAGCGCACCGGTTGCGAGAGGTGGGCTGTGGAGGGGTGGCCATTTT 840
Db 1441 CTCGCCCGGAGCGCACCGGTTGCGAGAGGTGGGCTGTGGAGGGGTGGCCATTTT 1500
QY 841 TGTCTAACCCTTAAGTGAAGAGGCGCTA 867
Db 1501 TGTCTAACCCTTAAGTGAAGAGGCGCTA 1527

RESULT 7
US-08-998-443-3

Sequence 3, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Funk, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-998-443-3

Query Match 97.9%; Score 848.6; DB 3; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1,2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGTACTCAGGAGGCTGAGACAGCAAGTCCGTTGAACCCGGGAGGCAAGTGTGAGTG 60
Db 662 AGTACTCAGGAGGCTGAGACAGCAAGTCCGTTGAACCCGGGAGGCAAGTGTGAGTG 720
QY 61 AGCCGAGATCAGCGCAGTACAGCTCCATCCACCGTGGGGAAGCAAGACTCCGTCGA 120
Db 721 AGCCGAGATCAGCGCAGTACAGCTCCATCCACCGTGGGGAAGCAAGACTCCGTCGA 780
QY 121 AAAAAAAAAATGTTACAAATTTATGTGGATTACTCCCTCTTTTACCCTCATCAAGACA 180
Db 781 AAAAAAAAAATGTTACAAATTTATGTGGATTACTCCCTCTTTTACCCTCATCAAGACA 840
QY 181 CAGACACTCTTTAAAGCAAGTCAATGTTAAAGCGCTTTCTTCTTAATAAAGGAG 240
Db 841 CAGACACTCTTTAAAGCAAGTCAATGTTAAAGCGCTTTCTTCTTAATAAAGGAG 900
QY 241 ATTGAGTCCCTTAAGATTAATTAATGAGTGTACCTTGATTAAGCATCCCTGCTCA 300
Db 901 ATTGAGTCCCTTAAGATTAATTAATGAGTGTACCTTGATTAAGCATCCCTGCTCA 960
QY 301 AGGAGAGCTGGAGAGGCAATTTCTAAGGAAAAAGGGGAGGTTGAACTCGAGCGCATC 360
Db 961 AGGAGAGCTGGAGAGGCAATTTCTAAGGAAAAAGGGGAGGTTGAACTCGAGCGCATC 1020
QY 361 CCATGAGCCGAGACAGATTTCTCTAGTCACTGCTGCTGGGAATCTAATTTTCAAA 420
Db 1021 CCATGAGCCGAGACAGATTTCTCTAGTCACTGCTGCTGGGAATCTAATTTTCAAA 1080
QY 421 AGTCTCCAAAAATGTGATGATCAAAAGTAATAGTGTGCTGTGCTTAGGCCCTA 480
Db 1081 AGTCTCCAAAAATGTGATGATCAAAAGTAATAGTGTGCTGTGCTTAGGCCCTA 1140

Qy	481	AAACCTTCGTGAATTTCCATTTTTTAAGGTAGCCAGGTAACCGCGCTCGTCTCGAGA	540
Db	1314	AAATCTTCGTGAATTCATTTTTTAAGGTAGTCGAGGTGAACCGCGTCTGCTCGAGA	1200
Qy	541	GGATAGCAAAAAAGGCCCTCGATACCTCAAGTATTAGTTTACCTTTAAAGAAAGTGCAG	600
Db	1201	GGATAGCAAAAAAGGCCCTCGATACCTCAAGTATTAGTTTACCTTTAAAGAAAGTGCAG	1260
Qy	601	TAAAGACGCAAAAGCTTTTCCCGGACGTGGGGAAGGCAACGTCTTCTCATATGGCCGAA	660
Db	1261	TAAAGACGCAAAAGCTTTTCCCGGACGTGGGGAAGGCAACGTCTTCTCATATGGCCGAA	1320
Qy	661	ATGGAACCTTAATTTTCCCGTTCCCGCCCAACACGCCGCCCGGAGAGTACTCTACAG	720
Db	1321	ATGGAACCTTAATTTTCCCGTTCCCGCCCAACACGCCGCCCGGAGAGTACTCTACAG	1380
Qy	721	AGCGCGAGAGTACGCTTTGGCCAAATCCGATGCGGTGGCGCGCGTCCCTTATAAGCGGA	780
Db	1381	AGCGCGAGAGTACGCTTTGGCCAAATCCGATGCGGTGGCGCGCGTCCCTTATAAGCGGA	1440
Qy	781	CTCGCCCGGAGCGCACCGGGTTGCCGAGGTTGGGCTTGGAGGGGTGGTGCCATTTTT	840
Db	1441	CTCGCCCGGAGCGCACCGGGTTGCCGAGGTTGGGCTTGGAGGGGTGGTGCCATTTTT	1500
Qy	841	TGCTTAACCTTAAGTGAAGAGCGCTGA	867
Db	1501	TGCTTAACCTTAAGTGAAGAGCGCTGA	1527

RESULT 8
US-09-060-523-3
Sequence 3, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villepoiteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2426 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;
US-09-0650-523-3

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Query Match      97.9%; Score 848.6; DB 4; Length 2426;
Best Local Similarity 99.4%; Pred. NO. 1.2e-253;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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QY	1	AGCTCTAGAGAGGCTGACGACGAGAAATGCTTTGAACCCGGGAGGACAGAGGTTCCACTG	60
Db	662	AGCTACTGAGGAGGCTGAGACACAGCAATGCTTTGAACCCGGGA-GCAGAGTTTCAAGTG	720
QY	61	AGCCGAGATCAGCGCCACTAGCTCATCCAGCCTGGGGCAAAAGAGCAAGCACTCCGTCA	120
Db	721	AGCCGAGATCAGCGCCACTAGCTCATCCAGCCTGGGGCAAAAGCAAGCACTCCGTCA	780
QY	121	AAAAAAAAATCGTTACAAATTTATGTTGGATTACTGCCCTCTTTTACTCATCAAGCA	180
Db	781	AAAAAAAAATCGTTACAAATTTATGTTGGATTACTGCCCTCTTTTACTCATCAAGCA	840
QY	181	CAGCACTACTTTAAAGCAAAATGCAATGATTGAACGCCCTTCTTCTTAATAAAGGAG	240
Db	841	CAGCACTACTTTAAAGCAAAATGCAATGATTGAACGCCCTTCTTCTTAATAAAGGAG	900
QY	241	ATTCACTCTTTAAGATTAAATATGTAGTACTTAACCTTAATTAAGCCATCTGTCTCA	300
Db	901	ATTCACTCTTTAAGATTAAATATGTAGTACTTAACCTTAATTAAGCCATCTGTCTCA	960
QY	301	AGGAGAACTCTGAGAAAGGCATTCTTAAGGAAAAAGGGGCAAGGGTTGGAATCTGGAGCA	360
Db	961	AGGAGAGGCTCTGAGAAAGGCATTCTTAAGGAAAAAGGGGCAAGGGTTGGAATCTGGAGCA	1020
QY	361	CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAAGTCTCCTCGGAAATCTAATTTTCACAA	420
Db	1021	CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAAGTCTCCTCGGAAATCTAATTTTCACAA	1080
QY	421	AGTTCTCCAAAAAATGTGATGATCAAAACCTAGAAATTAATGTTCTGTGCTTAGAGCCCTA	480
Db	1081	AGTTCTCCAAAAAATGTGATGATCAAAACCTAGAAATTAATGTTCTGTGCTTAGAGCCCTA	1140
QY	481	AAATCTTCCTGTGAATTCCAATTTTAAAGTAGTCGAGAGTGAACCGGCTGTGCTGACGA	540
Db	1141	AAATCTTCCTGTGAATTCCAATTTTAAAGTAGTCGAGAGTGAACCGGCTGTGCTGACGA	1200
QY	541	GGATAGAAAAAGGCCCTGTGATPACTCAAGTTAGTTTCACCTTTAAAGAAAGTCGGAG	600
Db	1201	GGATAGAAAAAGGCCCTGTGATPACTCAAGTTAGTTTCACCTTTAAAGAAAGTCGGAG	1260
QY	601	TAAAGAGCCCAAAAGCTTTCCCGGACGTGGGGAAGGGCAAGTCCTTCATAGGCGCGGA	660
Db	1261	TAAAGAGCCCAAAAGCTTTCCCGGACGTGGGGAAGGGCAAGTCCTTCATAGGCGCGGA	1320
QY	661	ATGGAATTTAATTTCCCGTTCCCGCCCAACAGCCCGCCCGGAGAGAGTACTCTACAGAG	720
Db	1321	ATGGAATTTAATTTCCCGTTCCCGCCCAACAGCCCGCCCGGAGAGAGTACTCTACAGAG	1380
QY	721	AGCCGCGAGATCAAGCTTTGGCCAAATCCGTGCGGTGGGGCGGCTCCTTTATTAAGCCGA	780
Db	1381	AGCCGCGAGATCAAGCTTTGGCCAAATCCGTGCGGTGGGGCGGCTCCTTTATTAAGCCGA	1440
QY	781	CTCGCCGCGAGCCACACCGGGTTGCGGAGAGGTGGGCTCGGAGAGGTGTGGCCATTTTT	840
Db	1441	CTCGCCGCGAGCCACACCGGGTTGCGGAGAGGTGGGCTCGGAGAGGTGTGGCCATTTTT	1500
QY	841	TGCTTAACCTTAAGTGAAGAGGCGCTA	867
Db	1501	TGCTTAACCTTAAGTGAAGAGGCGCTA	1527

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RESULT 9
US-08-485-778-1
; Sequence 1, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millita Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ. ID NO.: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-485-778-1

Query Match          96.3%; Score 834.6; DB 2; Length 2425;
Best Local Similarity 99.0%; Pred. No. 3,9e-259;
Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;
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DB 841 CAGCACTACTTTAAAGCAAGTCATGATTGAAGCGCTTTCTTCTAATAAAGGAG 900
QY 241 ATTACAGTCCTTAAGATTAAATATCTAGTAGTTACACTTGTATTAACCATCTCTCTA 300
DB 901 ATTACAGTCCTTAAGATTAAATATCTAGTAGTTACACTTGTATTAACCATCTCTCTA 960
QY 301 AGGAGAAGCTGGAGAGGCACTTAAAGGAAAAAGGGGAGGGTGGAGACTCGGAGCAGTC 360
DB 961 AGGAGAGGCTGGAGAGGCACTTAAAGGAGAAAGGGGAGGGTAGAGAACTCGGAGCAGTC 1020
QY 361 CCACGTAGCCGAGACAAAGATTCGTGTAGTCAAGTCTGCTCGGGAATCTATTTTCACAA 420
DB 1021 CCACGTAGCCGAGACAAAGATTCGTGTAGTCAAGTCTGCTCGGGAATCTATTTTCACAA 1080
QY 421 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTAAGTGTCTGTCTTAAGCCCTTA 480
DB 1081 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTAAGTGTCTGTCTTAAGCCCTTA 1140
QY 481 AAATCTTCCGTGATTCATTTTAAAGTAGTGAAGTGAACCGGCTGGTGTGTCGAGA 540
DB 1141 AAATCTTCCGTGATTCATTTTAAAGTAGTGAAGTGAACCGGCTGGTGTGTCGAGA 1200
QY 541 GGATAGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTTAAAGAGGTGCGAAG 600
DB 1201 GGATAGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTTAAAGAGGTGCGAAG 1260
QY 601 TAAAGACGAAGACCTTTCCCGGAGCTGGGGAAGGCAACGTCTTCTCATGCGCGGA 660
DB 1261 TAAAGACGAAGACCTTTCCCGGAGCTGGGGAAGGCAACGTCTTCTCATGCGCGGA 1320
QY 661 ATGGAACCTTTAATTTCCCGTCCCGCCCAACGAGCCCGCGAGAGAGTCACTGTCAGAG 720
DB 1321 ATGGAACCTTTAATTTCCCGTCCCGCCCAACGAGCCCGCGAGAGTCACTGTCAGAG 1380
QY 721 AGCCGCGAGAGTCAGCTTGAGCAATCGTGCCTGCGCGCGCTCCCTTTTAAAGCCGA 780
DB 1381 AGCCGCGAGAGTCAGCTTGAGCAATCGTGCCTGCGCGCGCTCCCTTTTAAAGCCGA 1440
QY 781 CTCGCCCGGAGCGCACCGGGTTGC---GAGAGGTGGGCTTGGGAGGGGTGTGGCCAT 836
DB 1441 CTCGCCCGGAGCGCACCGGGTTGC---GAGAGGTGGGCTTGGGAGGGGTGTGGCCAT 1500
QY 837 TTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 1501 TTTTGTCTAACCTTAAGTGAAGGGCGTA 1531

RESULT 10
US-08-520-550A-1
; Sequence 1, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millita Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-550A-1

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Query Match          96.3%; Score 834.6; DB 3; Length 2425;
Best Local Similarity 99.0%; Pred. No. 3,9e-259;
Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

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QY 1 AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAACCCCGGAGGAGGTTGCGATG 60
    |||||||
DB 662 AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAACCCCGGAGGAGGTTGCGATG 720
    |||||||
QY 61 AGCCGAGATCAGCGCACTTAACCTCCAGCCGCGGAGGAGGAGGAGGAGGAGGAGG 120
    |||||||
DB 721 AGCCGAGATCAGCGCACTTAACCTCCAGCCGCGGAGGAGGAGGAGGAGGAGGAGG 780
    |||||||
QY 121 AAAAAAAAAAATCGTTACAAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAGACA 180
    |||||||
DB 781 AAAAAAAAAAATCGTTACAAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAGACA 840
    |||||||
QY 181 CAGCAGCTTAAAGCAAGTCAATGATGAAAGCGCTTTCTTCTAATTAAGGAGGAG 240
    |||||||
DB 841 CAGCAGCTTAAAGCAAGTCAATGATGAAAGCGCTTTCTTCTAATTAAGGAGGAGGAG 900
    |||||||
QY 241 ATTCACTCTTAAGATTAATATGATGATTTACCTTGAATTAAGGAGGAGGAGGAGGAG 300
    |||||||
DB 901 ATTCACTCTTAAGATTAATATGATGATTTACCTTGAATTAAGGAGGAGGAGGAGGAG 960
    |||||||
QY 301 AGGAGAGCTGAGAGAGCAATCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
    |||||||
DB 961 AGGAGAGCTGAGAGAGCAATCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
    |||||||
QY 361 CCACTGAGCGGAGAGCAATCTTCTGCTAGTCACTGCTGCGGAGGAGGAGGAGGAGGAG 420
    |||||||
DB 1021 CCACTGAGCGGAGAGCAATCTTCTGCTAGTCACTGCTGCGGAGGAGGAGGAGGAGGAG 1080
    |||||||
QY 421 AGTTCTCAAAAAATGATGATCAAAATAGGAAATAGTGTCTGTGCTTAAAGGCGCTTA 480
    |||||||
DB 1081 AGTTCTCAAAAAATGATGATCAAAATAGGAAATAGTGTCTGTGCTTAAAGGCGCTTA 1140
    |||||||
QY 481 AAATCTTCTGTAATTCATTTTAAAGTAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
    |||||||
DB 1141 AAATCTTCTGTAATTCATTTTAAAGTAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
    |||||||
QY 541 GGATAGAAAAAGGCGCTGATACCTCAAGTTAGTTTCACTTTTAAAGAGGAGGAGGAGGAG 600
    |||||||
DB 1201 GGATAGAAAAAGGCGCTGATACCTCAAGTTAGTTTCACTTTTAAAGAGGAGGAGGAGGAG 1260
    |||||||

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QY 601 TAAAGACGAAAGCCCTTCCCGGAGCGTGGCGAAGGCGAACGCTCTTCTCATGCGCGAA 660
    |||||||
DB 1261 TAAAGACGAAAGCCCTTCCCGGAGCGTGGCGAAGGCGAACGCTCTTCTCATGCGCGAA 1320
    |||||||
QY 661 ATGGAACCTTTAATTTCCCGTTCGCCCAACACGCGCGCGGAGAGAGTCACTCAACGAG 720
    |||||||
DB 1321 ATGGAACCTTTAATTTCCCGTTCGCCCAACACGCGCGCGGAGAGAGTCACTCAACGAG 1380
    |||||||
QY 721 AGCCGAGAGTCAAGCTTGGCAATCCGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
    |||||||
DB 1381 AGCCGAGAGTCAAGCTTGGCAATCCGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
    |||||||
QY 781 CTCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 836
    |||||||
DB 1441 CTCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
    |||||||
QY 837 TTTTGTCTAACCTTAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 867
    |||||||
DB 1501 TTTTGTCTAACCTTAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1531
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RESULT 11
US-08-714-482-2
Sequence 2, Application US/08714482
Patent No. 5972605
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: Assays for Regulators of Mammalian
TITLE OF INVENTION: Telomerase Expression
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,482
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/521,634
FILING DATE: 31-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0086005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY:
LOCATION: 1..981
OTHER INFORMATION: /note="PsiI fragment containing htr"
OTHER INFORMATION: sequence"
US-08-714-482-2

Query Match      38.5%; Score 334; DB 2; Length 981;
Best Local Similarity 100.0%; Pred. No. 8e-98;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 CTCGAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAGG 593
DB 1 CTCGAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAGG 60
QY 594 TCGGAATTAAGACGCAAGCCTTTCCCGACGTCGGAAGGGCAAGCTCCTCATG 653
DB 61 TCGGAATTAAGACGCAAGCCTTTCCCGACGTCGGAAGGGCAAGCTCCTCATG 120
QY 654 GCCGGAATGAACCTTAATTTCCGTTCCCGCCCAACACGCGCCCGAGAGATGACTC 713
DB 121 GCCGGAATGAACCTTAATTTCCGTTCCCGCCCAACACGCGCCCGAGAGATGACTC 180
QY 714 TCACGAGAGCGCGAGAGTCAAGTTCGCAATCCGTGCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGAGCGCGAGAGTCAAGTTCGCAATCCGTGCGGCGCGCTCCCTTTAT 240
QY 774 AACCGACTCGCCCGGACGCGACCGGGTTGCGAGAGGTGGGCTGGAGGGGAGTGGC 833
DB 241 AACCGACTCGCCCGGACGCGACCGGGTTGCGAGAGGTGGGCTGGAGGGGAGTGGC 300
QY 834 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 867
DB 301 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 334

RESULT 12
US-08-710-249-5
Sequence 5, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Methods and Reagents for Regulating
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00122005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc-RNA
LOCATION: 267..715
OTHER INFORMATION:
OTHER INFORMATION: /product="htr"
OTHER INFORMATION: /note="htr transcript serves as
template in the telomerase
OTHER INFORMATION: ribonucleoprotein"
US-08-710-249-5

Query Match      38.4%; Score 333; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.7e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTCGAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAGG 593
DB 1 CTCGAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAGG 60
QY 594 TCGGAATTAAGACGCAAGCCTTTCCCGACGTCGGAAGGGCAAGCTCCTTCATG 653
DB 61 TCGGAATTAAGACGCAAGCCTTTCCCGACGTCGGAAGGGCAAGCTCCTTCATG 120
QY 654 GCCGGAATGAACCTTAATTTCCGTTCCCGCCCAACACGCGCCCGAGAGATGACTC 713
DB 121 GCCGGAATGAACCTTAATTTCCGTTCCCGCCCAACACGCGCCCGAGAGATGACTC 180
QY 714 TCACGAGAGCGCGAGAGTCAAGTTCGCAATCCGTGCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGAGCGCGAGAGTCAAGTTCGCAATCCGTGCGGCGCGCTCCCTTTAT 240
QY 774 AACCGACTCGCCCGGACGCGACCGGGTTGCGAGAGGTGGGCTGGAGGGGAGTGGC 833
DB 241 AACCGACTCGCCCGGACGCGACCGGGTTGCGAGAGGTGGGCTGGAGGGGAGTGGC 300
QY 834 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 867
DB 301 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 334

RESULT 13
US-09-220-157A-5
Sequence 5, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Methods and Reagents for Regulating
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,157A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00122005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ. ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 267..715
; OTHER INFORMATION: /note="hmr transcript serves as
; OTHER INFORMATION: template in the telomerase
; OTHER INFORMATION: ribonucleoprotein"
; US-09-220-157A-5

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Query Match      38.4%; Score 333; DB 4; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.7e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATAGAAAAAGAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 593
DB 1 CTGCAGAGATAGAAAAAGAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
QY 594 TCGGAAGTAAAGAGCGCAAGCCTTTCCCGAGCGTGGGGAAGGCGAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGAGCGCAAGCCTTTCCCGAGCGTGGGGAAGGCGAACGTCCTTCATG 120
QY 654 GCGGGAATGGAACCTTAATTTCCCGTCCCGCAACAGCCGCGCGAGAGTGACTC 713
DB 121 GCGGGAATGGAACCTTAATTTCCCGTCCCGCAACAGCCGCGCGAGAGTGACTC 180
QY 714 TCACGAGAGCGGAGAGTACGCTGGGCAATCGTGCGGTCGCGCGCCCTCCCTTAT 773
DB 181 TCACGAGAGCGGAGAGTACGCTGGGCAATCGTGCGGTCGCGCGCCCTCCCTTAT 240
QY 774 AAGCGACTGCCCGGAGCGACCGGTTGCGGAGGTTGGGCTGGGAGGGTGTGGC 833
DB 241 AAGCGACTGCCCGGAGCGACCGGTTGCGGAGGTTGGGCTGGGAGGGTGTGGC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 334

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RESULT 14
US-08-770-565-1
; Sequence 1, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo

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; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; TELEFAX: 415-576-0200
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-565-1

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Query Match      38.3%; Score 332.4; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.6e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 CTGCAGAGATAGAAAAAGAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
QY 594 TCGGAAGTAAAGAGCGCAAGCCTTTCCCGAGCGTGGGGAAGGCGAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGAGCGCAAGCCTTTCCCGAGCGTGGGGAAGGCGAACGTCCTTCATG 120
QY 654 GCGGGAATGGAACCTTAATTTCCCGTCCCGCAACAGCCGCGCGAGAGTGACTC 713
DB 121 GCGGGAATGGAACCTTAATTTCCCGTCCCGCAACAGCCGCGCGAGAGTGACTC 180
QY 714 TCACGAGAGCGGAGAGTACGCTGGGCAATCGTGCGGTCGCGCGCCCTCCCTTAT 773
DB 181 TCACGAGAGCGGAGAGTACGCTGGGCAATCGTGCGGTCGCGCGCCCTCCCTTAT 240
QY 774 AAGCGACTGCCCGGAGCGACCGGTTGCGGAGGTTGGGCTGGGAGGGTGTGGC 833
DB 241 AAGCGACTGCCCGGAGCGACCGGTTGCGGAGGTTGGGCTGGGAGGGTGTGGC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 334

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RESULT 15
US-08-833-377-1
; Sequence 1, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:

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APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..981
OTHER INFORMATION: /note="PsiI fragment of the 2.4 kb
OTHER INFORMATION: SauIIIAI-HindIII fragment of clone 28-1"
US-08-833-377-1

Query Match 38.3%; Score 332.4; DB 2; Length 981;
Best local Similarity 99.7%; Pred. No. 2.6e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 594 TCGGAGTAAGACGCAACGCTTCCCGAGCGCGGAGGCAAGCGTCCTTCATG 653
DB 61 TCGGAGTAAGACGCAACGCTTCCCGAGCGCGGAGGCAAGCGTCCTTCATG 120
QY 654 GCCGGAATGGAATTAATTTCCCGTCCCGCAACACAGCCCGCCGAGAGTGAATC 713
DB 121 GCCGGAATGGAATTAATTTCCCGTCCCGCAACACAGCCCGCCGAGAGTGAATC 180
QY 714 TCACGAGAGCGCGAGAGTCAAGCTTGCCCAATCGTGGGTGCGGCGCGCTCCCTTAT 773
DB 181 TCACGAGAGCGCGAGAGTCAAGCTTGCCCAATCGTGGGTGCGGCGCGCTCCCTTAT 240
QY 774 AAGCCGACTCGCCCGCAGCGCAACCGGTTGCGGAGGTTGGGCTGGGAGGGTGGTGGC 833
DB 241 AAGCCGACTCGCCCGCAGCGCAACCGGTTGCGGAGGTTGGGCTGGGAGGGTGGTGGC 300
QY 834 CATTTTGTCTAACCTAAGAGGCGTA 867

DB 301 CATTTTGTCTAACCTAAGAGGCGTA 334

Search completed: January 25, 2003, 13:43:36
Job time: 95 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:43:40 ; Search time 3208 Seconds

7865.378 Million cell updates/sec

Title: US-09-601-267-36

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 41: em.hgo.other:*

Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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C 4	860.6	99.3	145829	2	AC076802	AC076802 Homo sapi
	848.6	97.9	2420	6	I131750	I131750 Sequence 3
	848.6	97.9	2426	6	AR016035	AR016035 Sequence
	848.6	97.9	2426	6	AR059196	AR059196 Sequence
	848.6	97.9	2426	6	AR075507	AR075507 Sequence
7	848.6	97.9	2426	6	AR081664	AR081664 Sequence
8	848.6	97.9	2426	6	AR161905	AR161905 Sequence
9	848.6	97.9	2426	6	AR081665	AR081665 Sequence
10	848.6	97.9	981	6	AR028774	AR028774 Sequence
11	334	38.4	981	6	AR022166	AR022166 Sequence
12	333	38.4	981	6	AB4591	AB4591 Sequence 1
13	333	38.3	981	6	AR063825	AR063825 Sequence
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18	166	19.1	548	9	AX019627	AX019627 Sequence
19	163	18.8	545	9	AC004888	AC004888 Homo sapi
20	120	13.8	120	6	AC113136	AC113136 Homo sapi
21	117.2	13.5	157466	6	AC024240	AC024240 Homo sapi
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23	115.6	13.3	165105	2	AC073341	AC073341 Homo sapi
24	114.2	13.2	197095	9	AL356536	AL356536 Homo sapi
25	114	13.1	115812	9	AC058396	AC058396 Homo sapi
26	113.6	13.1	176550	9	AC067969	AC067969 Homo sapi
27	112.6	13.0	39170	9	AC002542	AC002542 Human BAC
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29	110.8	12.8	68275	9	AC012614	AC012614 Homo sapi
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31	110.8	12.8	187495	9	AC073341	AC073341 Homo sapi
32	110.6	12.8	185574	9	AL122004	AL122004 Human DNA
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34	110	12.7	132912	9	AC091328	AC091328 Homo sapi
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36	109.4	12.6	123437	9	AC117507	AC117507 Homo sapi
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38	109.4	12.6	148505	9	AC066603	AC066603 Homo sapi
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40	109.4	12.6	211452	2	AL133516	AL133516 Human DNA
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ALIGNMENTS

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ACCESSION	AX019582			
VERSION	AX019582.1	GI:10043496		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
TITLE	1 (bases 1 to 867)			
	Kelth, W.N.			
	promoter regions of the mouse and human telomerase rna component			
	genes			

JOURNAL	Patent: WO 9938964-A 36 05-AUG-1999:			
FEATURES	KEITH WILLIAM NICOL (GB): CANCER RES			
source	Location/Qualifiers			
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	/db_xref="taxon:9606"			
BASE COUNT	237 a	209 c	231 g	200 t
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Best Local Similarity	100.0%;	Pred. No. 5.5e-240;		
Matches 867;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

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Db 1 AGCTACTCAGGAGCGCTGAGACACGAGAATCGTTGAAACCCGGGAGGACAGGTTGCAGTG 60

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QY 121 AAAAAAAAAATCGTTACATTTATGGTGGATTAACCTCCCTCTTTTACCTCATCAAGACA 180

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Qy	181	CAGCGTACTTTAAAGCAAGTCATATTTGAAGCGCTTTCTTTCTAATTAAGGAG	240
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Qy	241	ATTAGAGCCTTTAGATTAATTAATTAATCTAGTAACTTGAATTAAGGCATCCTCTGCA	300
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RESULT 2			
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LOCUS	AX019547	1765 bp	DNA
DEFINITION	Sequence 1 from Patent WO9338564.		linear
ACCESSION	AX019547		
VERSION	AX019547.1	GI:10043461	PAT 07-SEP-2000

ORGANISM	REFERENCE
Homo sapiens	1 (bases 1 to 1755)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

TITLE	Promoter regions of the mouse and human telomerase rna component
JOURNAL	genes
FEATURES	Patent: WO 9938964-A 1 05-AUG-1999; KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
SOURCE	Location/Qualifiers 1..1765

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BASE COUNT      404 a      458 c      480 g      423 t
ORIGIN
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Query Match	100.0%;	Score 867;	DB 6;	length 1765;
Best Local Similarity	100.0%;	Pred. No. 6.2e-240;		
Matches 867; Conservative	0;	Mismatches	0;	Gaps 0;

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Db	1	AGCTACTCAGGAGGCTGTGACACAGAGAAATCGCTTTGAACCCGGGAGGCGAGAGTTGCAGTG	60
QY	61	AGCGGAGATCAGCGCCACTAGACTCCATTCACGCTCGGGGGAAGAAGCAGCAAGCTCCGTCTCA	120
Db	61	AGCGGAGATCAGCGCCACTAGACTCCATTCACGCTCGGGGGAAGAAGCAGCAAGCTCCGTCTCA	120

QY	121	AAAAAAAACGTTACAACTTAAGTGGAGTACTCCGCCCTTTTACGTCACACACA	180
Db	121	AAAAAAAAACGTTACATTTAGTGGATTACTCCGCCCTTTTACGTCACACACA	180
QY	181	CAGCACTCTTTAAGCAAAATCATGATTGAACGCCCTTCTTCTTAATTAAGGGAG	240
Db	181	CAGCACTCTTTAAGCAAAATCATGATTGAACGCCCTTCTTCTTAATTAAGGGAG	240

QY	241	ATTAGTCTTAAATTAATTAATAGTACGTTAAAGCATCTCTGCTCA	300
Dp	241	ATTAGTCTTAAATTAATTAATAGTACGTTAAAGCATCTCTGCTCA <td>300</td>	300
QY	301	AGGAGAACTCGAGAAGCAATTAAAGAAAAAGGGCAGGGTGCNACTCGGACGCATC <td>360</td>	360
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QY	421	AGTCTCCAAAAATGTGATGATCAAAACATAGGAATTAAGTCTGTGTTTAGGCCCTA	480
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QY	361	CCACTGAGCCGACGAAGATTCTCTCTAGTCACTGCTGCTGGGATCTATTATTTCCAA	420

QY	Db
541	481
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6000	5400

QY	601	TAAAGACGCAAAAGCCTTCCCGGACGTGGCGAAGGCAACGTCCTTCATGATGGCGGAA	650
Db	601	TAAAGACGCAAAAGCCTTCCCGGACGTGGCGAAGGCAACGTCCTTCATGATGGCGGAA	650

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QY 721 AGCCGAGAGTACAGTTGGCCCAATCCGTGCGGCGGCGCTCCCTTATTAAGCGA 780
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Db 721 AGCCGAGAGTACAGTTGGCCCAATCCGTGCGGCGGCGCTCCCTTATTAAGCGA 780
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QY 841 TGTCTAACCTTAAGTGAAGGCGCTA 867
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Db 841 TGTCTAACCTTAAGTGAAGGCGCTA 867

RESULT 3
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LOCUS AF047386 Homo sapiens telomerase RNA (TR) gene, promoter and complete
DEFINITION sequence.
ACCESSION AF047386 GI:300555
VERSION AF047386.1
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1765)
AUTHORS Black,J.O., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
Black,D.M. and Keith,W.N.
TITLE Cloning and characterization of human and mouse telomerase RNA gene
promoter sequences
JOURNAL Oncogene 16 (10), 1345-1350 (1998)
MEDLINE 98206512
PUBMED 9546436
REFERENCE 2 (bases 1 to 1765)
AUTHORS Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
Black,D.M. and Keith,W.N.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1998) Medical Oncology, Beatson Institute,
Switchback Rd, Glasgow G61 1BD, UK
FEATURES
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/chromosome="3"
/map="3q26.3"
1..1248
/gene="TR"
1..798
/promoter="TR"
799..1248
/misc_RNA
/feature="telomerase RNA"
BASE COUNT 404 a 458 c 480 g 423 t
ORIGIN
Query Match 100.0%; Score 867; DB 9; Length 1765;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTACTCAGGAGGTGAGACAGAGAAATCGTTGAACCGGGAGCAGAGTTGCAGTG 60
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Db 1 AGTACTCAGGAGGTGAGACAGAGAAATCGTTGAACCGGGAGCAGAGTTGCAGTG 60
QY 61 AGCCGAGATCACCCACTACACTCATCCAGCCTGGGCGAAGAAGCAAGACTCCGTCTCA 120
|||||
Db 61 AGCCGAGATCACCCACTACACTCATCCAGCCTGGGCGAAGAAGCAAGACTCCGTCTCA 120
QY 121 AAAAAAAAAATCGTTCATTTATGTGTGATTAAGTCTCCCTCTTTTAACTCATCAAGACA 180
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QY 181 CACACTACTTTTAAAGCAAGTCAATGATTAAGAACCCCTTTCTTTCTATAAAGGAG 240
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QY 241 ATTCACTCTTAAGATTAATATGATGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
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QY 301 AGGAGAGGTGGAGAGGATCTTAAGGAAAAAGGGGCGAGGTTGAAGTGAAGTGAAGTGAAG 360
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Db 301 AGGAGAGGTGGAGAGGATCTTAAGGAAAAAGGGGCGAGGTTGAAGTGAAGTGAAGTGAAG 360
QY 361 CCACGTAGCGGAGACAAAGATTTCTGTAGTCAAGTCTCTCTGGAATCAATTTTACAA 420
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Db 361 CCACGTAGCGGAGACAAAGATTTCTGTAGTCAAGTCTCTCTGGAATCAATTTTACAA 420
QY 421 AGTTCTCAAAAAATGTGATCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
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Db 421 AGTTCTCAAAAAATGTGATCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
QY 481 AATCTTCTCTGAATTTTCAATTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540
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Db 661 ATGGAATTATTTCCCTTCCCAACACACCCCGGAGAGTACTCTACAGAG 720
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Db 721 AGCCGAGAGTACAGTTGGCCCAATCCGTGCGGCGGCGCTCCCTTATTAAGCGA 780
QY 781 CTCGCCCGGACGACACCGGGTTGCGAGGGTGGCGCTGGAGGGGTGTGCCATTTT 840
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Db 781 CTCGCCCGGACGACACCGGGTTGCGAGGGTGGCGCTGGAGGGGTGTGCCATTTT 840
QY 841 TGTCTAACCTTAAGTGAAGGCGCTA 867
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Db 841 TGTCTAACCTTAAGTGAAGGCGCTA 867

RESULT 4
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LOCUS AC078802 Homo sapiens chromosome 3 clone RP11-816u6, WORKING DRAFT SEQUENCE,
DEFINITION 2 unordered pieces.
ACCESSION AC078802
VERSION AC078802.11 GI:21397225
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 145829)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., AmaralLunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL
Delaney, K. R., Delgado, O., Dem, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Dudin, K. J., Eunhardt, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gaisli, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homs, J. F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudas, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lounsged, H., Locado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maleshtwar, M., Mapua, P., Math, R., Martindale, A., Martinez, E., Massey, E., McWhirley, E., McLeod, M. P., Meador, M., Mel, G., Metzger, M., Miner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nockemko, S., Ogun, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I., Sodegren, E., Soneike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Teitrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlarczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorilla, S., Nelson, D., Weinstock, G., and Gibbs, R.	Direct Submission Unpublished 2 (bases 1 to 145829) Worley, K. C. Direct Submission Submitted (04-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 145829) Worley, K. C. Direct Submission Submitted (19-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 13, 2002 this sequence version replaced gi:20514648.	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Drafting Center Code: BCM Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: HBT Center clone name: RP11-816J6 Summary Statistics Sequencing vector: M13; Chemistry: Dye-terminator Big Dye; 65% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 145499 bases at least Q40 Consensus quality: 145597 bases at least Q40 Consensus quality: 145599 bases at least Q20 Estimated insert size: 148612; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Drafting Center Code: BCM Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: HBT Center clone name: RP11-816J6 Summary Statistics Sequencing vector: M13; Chemistry: Dye-terminator Big Dye; 65% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 145499 bases at least Q40 Consensus quality: 145597 bases at least Q40 Consensus quality: 145599 bases at least Q20 Estimated insert size: 148612; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Drafting Center Code: BCM Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: HBT Center clone name: RP11-816J6 Summary Statistics Sequencing vector: M13; Chemistry: Dye-terminator Big Dye; 65% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 145499 bases at least Q40 Consensus quality: 145597 bases at least Q40 Consensus quality: 145599 bases at least Q20 Estimated insert size: 148612; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

	* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.	
	1 8300: contig of 8300 bp in length	
	* 8301 8400: gap of unknown length	
	* 8401 145829: contig of 137423 bp in length.	
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	/clone="RP11-816J5"	
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OY	361 CCAGTAGCCGAGACAAGATTCGCTGTAGTCAGTGCCTCCGGGAATCTAATTTTCACAA 420	
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OY	421 AGTTCTCCAATAAATGTGATGATCAAAACTAGGAATTAGTGTCTGTCTTAAGGCCCTA 480	
Db 143573	AGTTCTCCAATAAATGTGATGATCAAAACTAGGAATTAGTGTCTGTCTTAAGGCCCTA 143514	
OY	481 AAATCTTCCTGGATTCOCATTTTAAAGTATGCGAGGGAACCGCGTCTGTGCGACA 540	
Db 143513	AAATCTTCCTGGATTCOCATTTTAAAGTATGCGAGGGAACCGCGTCTGTGCGACA 143454	
OY	541 GGATGAAAAAAGGCCCTCTGTATACCTCAAGTTAGTTTACCCTTTAAAGAAAGTGGAG 600	
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Db 143273	AGCCCGAGAGATCACCTTGGCCAAATCCGTGGCGGTGGGCGGCGCTCTTATTAAGCCGA 143214	
OY	781 CTCGCCGCGACGACCGGGGTTGGGGAAGGATGGGCTTGGGAAGGGGTGGGCCATTTTT 840	

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QY 841 TGTCTAACCTTAAGTGAAGGCGCTA 867
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LOCUS 131750 2420 bp DNA 1linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5583016.
ACCESSION 131750
VERSION 131750.1 GI:1822541
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2420)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5583016-A 3 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..2420
BASE COUNT 620 a 572 c 647 g 581 t
ORIGIN

Query Match 97.9%; Score 848.6; DB 6; Length 2420;
Best Local Similarity 99.4%; Pred. No. 1.4e-234;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 121 AAAAAAAAAATCGTTCAATTTATGGGATTACTCCCTTTTAACTCATCAAGACA 180
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QY 241 ATTCACTCTTAAAGATTAATATGTAAGTACTTACACTTGATTTAAAGCAATCTCTGCTCA 300
Db 901 ATTCACTCTTAAAGATTAATATGTAAGTACTTACACTTGATTTAAAGCAATCTCTGCTCA 960

QY 301 AGGAGAAAGCTGGAGAGGCAATTTCTAAGGAAAGAGGGGAGGGTTGGAACTCGGAGCATC 360
Db 961 AGGAGAGGCTGGAGAGGCAATTTCTAAGGAAAGAGGGGAGGGTGAAGCTCGGAGCATC 1020

QY 361 CCACTGAGCCGAGACAAGATTTCTGCTGTAAGTCAAGTCTGCTGGGAATCTAATTTTCACAA 420
Db 1021 CCACTGAGCCGAGACAAGATTTCTGCTGTAAGTCAAGTCTGCTGGGAATCTAATTTTCACAA 1080

QY 421 AGTTTCTCAAAAAATGATGATCAAAACTAGAAATTAGTGTCTGTGTTTAAAGGCGCTTA 480
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QY 481 AAATCTCTCTGTAATTCATATTTTAAAGTATGAGAGTGAACGGCTGTGATGCGAGA 540
Db 1141 AAATCTCTCTGTAATTCATATTTTAAAGTATGAGAGTGAACGGCTGTGATGCGAGA 1200

QY 541 GGATAGAAAAAGGCGCTGTGATACCTCAAGTTAGTTTCACTTTTAAAGAGTCCGAG 600
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QY 601 TAAAGAGCAAGGCTTCCCGGAGCTGGGAAAGGCAAGCTCTTCTATGCGCGGAA 660
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Db 1261 TAAAGAGCAAGGCTTCCCGGAGCTGGGAAAGGCAAGCTCTTCTATGCGCGGAA 1320
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QY 721 AGCCGAGAGTCAAGTTGGCCAATCCGTGGGTGGGCGCGCTCCCTTTATTAAGCCGA 780
Db 1381 AGCCGAGAGTCAAGTTGGCCAATCCGTGGGTGGGCGCGCTCCCTTTATTAAGCCGA 1440

QY 781 CTCGCCCGGAGCGACACCGGTTGCGGAGGTTGGGCTGGGAGAGGTTGGTGGCCATTTT 840
Db 1441 CTCGCCCGGAGCGACACCGGTTGCGGAGGTTGGGCTGGGAGAGGTTGGTGGCCATTTT 1500

QY 841 TGTCTAACCTTAAGTGAAGGCGCTA 867
Db 1501 TGTCTAACCTTAAGTGAAGGCGCTA 1527

RESULT 6
LOCUS AR016035 2426 bp DNA 1linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776679.
ACCESSION AR016035
VERSION AR016035.1 GI:3972312
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..2426
BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.9%; Score 848.6; DB 6; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.4e-234;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 ACCTACTCAGAGCGCTGAGACAGAGAAATCGCTTGAACCCGGAGCGAGAGTTGCAGTG 60
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QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGCGAAAGCAAGCACTCCGTCTCA 120
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QY 121 AAAAAAAAAATCGTTCAATTTATGGGATTACTCCCTTTTAACTCATCAAGACA 180
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QY 181 CACCACTACTTTAAAGCAAAATGATGTAAGCAAGCGCTTCTTCTCTAATAAAGGAG 240
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QY 361 CCACTGAGCCGAGACAAGATTTCTGCTGTAAGTCAAGTCTGCTGGGAATCTAATTTTCACAA 420
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Qy	541	GGATGAAAAAAGGCCCTCTGTATACCTCAAGTTAGTTTACCTTTAAAGAAAGTTCGGAAG	600
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Qy	721	AGCCCGAGAGCTCAGACTTGGCCATTCGCTGGCGTGGCGGCCGCTCCCTTTAATAGCCGA	780
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[illegible]

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Db	961	AGGAGAGGCTGAGAGAGGCATCTTAAGGAGAAAGGGGCGAGGGTAAAGAACTCGAGCGCATC	1020
QY	361	CCACAGAGCCGAGACAAATCTGCTGTAGTCAGTGTCTGCTGGGAATCTATTTTACAA	420
Db	1021	CCACGAGCCGAGACAAATCTGCTGTAGTCAGTGTCTGCTGGGAATCTATTTTACAA	1080
QY	421	AGTTCTCCAAAAAATGTGATGATCAAAACTAGAAATTAGTGTCTGTCTTAAGGCCCTA	480
Db	1081	AGTTCTCCAAAAAATGTGATGATCAAAACTAGAAATTAGTGTCTGTCTTAAGGCCCTA	1140
QY	481	AAATCTCTCTGTGAATTCATTTTAAAGTAGTCAGGATGAACCGCTGTGCTGCAGA	540
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QY	541	GGATGAGAAAAAGGCCCTGCTGATACCTCAAGTAACTTTCACCTTTAAAGAGTGTGGAAG	600
Db	1201	GGATGAGAAAAAGGCCCTGCTGATACCTCAAGTAACTTTCACCTTTAAAGAGTGTGGAAG	1260
QY	601	TAAAGACGCAAAAGCCTTCCCGAGCTGCGGAAGGGCAAGCTCTCTCTCAATGCGCGAA	660
Db	1261	TAAAGACGCAAAAGCCTTCCCGAGCTGCGGAAGGGCAAGCTCTCTCTCAATGCGCGAA	1320
QY	661	ATGGAATCTTAATTTCCCGTTCCCGCCCAACGACGCCGCCGAGAGAGTGACTCTCACGAG	720
Db	1321	ATGGAATCTTAATTTCCCGTTCCCGCCCAACGACGCCGCCGAGAGAGTGACTCTCACGAG	1380
QY	721	AGCGCGAGAGCTACACTTGGCCAAATCGGTGGGTGCGGGCGGCTCCCTTAATAAGCCGA	780
Db	1381	AGCGCGAGAGCTACACTTGGCCAAATCGGTGGGTGCGGGCGGCTCCCTTAATAAGCCGA	1440
QY	781	CTCGCGCGGACGACGACCGGGGTTGGCGAGGGTGGGCTCTGGGAGAGGAGTGGGCCATTTT	840
Db	1441	CTCGCGCGGACGACGACCGGGGTTGGCGAGGGTGGGCTCTGGGAGAGGAGTGGGCCATTTT	1500
QY	841	TGCTTAACCTTAAGAGAGGGCGTA	867
Db	1501	TGCTTAACCTTAAGAGAGGGCGTA	1527

LOCUS	AR075507	2426 bp	DNA	linear	PAT 30-AUG-2000
DEFINITION	Sequence 1 from patent US 5958680.				
ACCESSION	AR075507				
VERSION	AR075507.1	GI:10002257			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2426)				
TITLE	Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.				
JOURNAL	Mammalian telomerase				
FEATURES	Patent: US 5958680-A 4 28-SEP-1999;				
	Location/Qualifiers				
	source				
	1..2426				
	/organism="unknown"				
BASE COUNT	620 a	575 c	650 g	581 t	
ORIGIN					
Query Match	97.9%;	Score 848.6;	DB 6;	Length 2426;	
Best Local Similarity	99.4%;	Pred. No. 1.4e-234;			
Matches 862; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1;	
QY	1 AGCTCTCAGGAGGCGTGAACACGAGATCGCTTGAACCGGGAGCGAGAGTTCGATG 60				
DB	662 AGCTACTAGGAGGGGTGAGACACGAGATCCCTTCAACCCGGGA-GCAGAGGTTGCATG 720				
QY	61 AGCCGAGATCAAGCCACTAGACTCCATCCAGCTGGCGGAAGAGCAAGACTCGTCTCA 120				

Db 721 AGCCGAGATCAGCCACTGATCCAGCCCTGGGCAAAAGAGACATCCGTCTCA 780
 QY 121 AAAAAAAAAATCGTTAAATTTATGGTATGATCTCCCTCTTTTAACTCATCAAGACA 180
 Db 781 AAAAAAAAAATCGTTAAATTTATGGTATGATCTCCCTCTTTTAACTCATCAAGACA 840
 QY 181 CAGCACTACTTTAAAGCAAAATGATTTGAAGCCCTTTCTTTCTATAAAAGGAG 240
 Db 841 CAGCACTACTTTAAAGCAAAATGATTTGAAGCCCTTTCTTTCTATAAAAGGAG 900
 QY 241 ATTCACTCTTAAAGTAAATATGATGATTTACTTGAATTAAGCCATCTCTCTCA 300
 Db 901 ATTCACTCTTAAAGTAAATATGATGATTTACTTGAATTAAGCCATCTCTCTCA 960
 QY 301 AGGAGAAGCTGAGAGAGCATTTCTAAGGAAAAAGGGGAGGGTGGAACTCGAGCATC 360
 Db 961 AGGAGAAGCTGAGAGAGCATTTCTAAGGAAAAAGGGGAGGGTGGAACTCGAGCATC 1020
 QY 361 CCACGTAGCCGAGACAAAGATTTCTGTAGTCAAGTGTGCTGGGAATCTATTTGACAA 420
 Db 1021 CCACGTAGCCGAGACAAAGATTTCTGTAGTCAAGTGTGCTGGGAATCTATTTGACAA 1080
 QY 421 AGTTCTCCAAAAATGATGATCAAAACCTAGAAATTAAGTGTCTGTCTTAAAGCCCTA 480
 Db 1081 AGTTCTCCAAAAATGATGATCAAAACCTAGAAATTAAGTGTCTGTCTTAAAGCCCTA 1140
 QY 481 AATCTTCTGTGATTTCAATTTTAAAGTATGAGTGAACCGGCTGTGCTGACAGA 540
 Db 1141 AATCTTCTGTGATTTCAATTTTAAAGTATGAGTGAACCGGCTGTGCTGACAGA 1200
 QY 541 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTGGGAAG 600
 Db 1201 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTGGGAAG 1260
 QY 601 TAAAGAGCAAAAGCTTTCCCGAGAGTGGGAAAGGCAAGCTCTTCTATGCGCGAA 660
 Db 1261 TAAAGAGCAAAAGCTTTCCCGAGAGTGGGAAAGGCAAGCTCTTCTATGCGCGAA 1320
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 Db 1321 ATGGAATTTAATTTCCCGTTCGCCCAACACGCGCGCGAGAGTGAAGTCTCAAGAG 1380
 QY 721 AGCCGAGAGTCAAGTGTGCAATCGTGGTGGCGGCGCGCTCCCTTTATAGCCGA 780
 Db 1381 AGCCGAGAGTCAAGTGTGCAATCGTGGTGGCGGCGCGCTCCCTTTATAGCCGA 1440
 QY 781 CTGCGCCGAGAGGCAACCGGGTGGGAGGCTGGGAGGGTGGTGGCCATTTT 840
 Db 1441 CTGCGCCGAGAGGCAACCGGGTGGGAGGCTGGGAGGGTGGTGGCCATTTT 1500
 QY 841 TGCTAACCTTAAGTGAAGGGCGTA 867
 Db 1501 TGCTAACCTTAAGTGAAGGGCGTA 1527
 RESULT 9
 ARO81664 LOCUS 2426 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 1 from patent US 5972605.
 ACCESSION ARO81664
 VERSION ARO81664.1 GI:10008390
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2426)
 AUTHORS Villeponteu, B. and Harley, C.
 TITLE Assays for regulators of mammalian telomerase expression
 JOURNAL Patent: US 5972605-A 1 26-OCT-1999.
 FEATURES
 source location/Qualifiers
 1..2426
 /organism="unknown"
 BASE COUNT 620 a 575 c 650 g 581 t

ORIGIN
 Query Match 97.9% Score 848.6; DB 6; Length 2426;
 Best Local Similarity 99.4% Pred. No. 1.4e-234;
 Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 1 AGCTACTCAGGAGGCTGAGACACGAGAAATCGTTGAACCCGGGAGGACAGAGTTGCAGTG 60
 Db 662 AGCTACTCAGGAGGCTGAGACACGAGAAATCGTTGAACCCGGGA -CCAGAGTTGAGTG 720
 QY 61 AGCCGAGATCAGGCCACTGATCCATCCAGCTGGGCGAAAGAGCAACATCCGTCTCA 120
 Db 721 AGCCGAGATCAGGCCACTGATCCATCCAGCTGGGCGAAAGAGCAACATCCGTCTCA 780
 QY 121 AAAAAAAAAATCGTTAAATTTATGGTATGATCTCCCTCTTTTAACTCATCAAGACA 180
 Db 781 AAAAAAAAAATCGTTAAATTTATGGTATGATCTCCCTCTTTTAACTCATCAAGACA 840
 QY 181 CAGCACTACTTTAAAGCAAAATGATTTGAAGCCCTTTCTTTCTATAAAAGGAG 240
 Db 841 CAGCACTACTTTAAAGCAAAATGATTTGAAGCCCTTTCTTTCTATAAAAGGAG 900
 QY 241 ATTCACTCTTAAAGTAAATATGATGATTTACTTGAATTAAGCCATCTCTCTCA 300
 Db 901 ATTCACTCTTAAAGTAAATATGATGATTTACTTGAATTAAGCCATCTCTCTCA 960
 QY 301 AGGAGAAGCTGAGAGAGCATTTCTAAGGAAAAAGGGGAGGGTGGAACTCGAGCATC 360
 Db 961 AGGAGAAGCTGAGAGAGCATTTCTAAGGAAAAAGGGGAGGGTGGAACTCGAGCATC 1020
 QY 361 CCACGTAGCCGAGACAAAGATTTCTGTAGTCAAGTGTGCTGGGAATCTATTTGACAA 420
 Db 1021 CCACGTAGCCGAGACAAAGATTTCTGTAGTCAAGTGTGCTGGGAATCTATTTGACAA 1080
 QY 421 AGTTCTCCAAAAATGATGATCAAAACCTAGAAATTAAGTGTCTGTCTTAAAGCCCTA 480
 Db 1081 AGTTCTCCAAAAATGATGATCAAAACCTAGAAATTAAGTGTCTGTCTTAAAGCCCTA 1140
 QY 481 AATCTTCTGTGATTTCAATTTTAAAGTATGAGTGAACCGGCTGTGCTGACAGA 540
 Db 1141 AATCTTCTGTGATTTCAATTTTAAAGTATGAGTGAACCGGCTGTGCTGACAGA 1200
 QY 541 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTGGGAAG 600
 Db 1201 GGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTGGGAAG 1260
 QY 601 TAAAGAGCAAAAGCTTTCCCGAGAGTGGGAAAGGCAAGCTCTTCTATGCGCGAA 660
 Db 1261 TAAAGAGCAAAAGCTTTCCCGAGAGTGGGAAAGGCAAGCTCTTCTATGCGCGAA 1320
 QY 661 ATGGAATTTAATTTCCCGTTCGCCCAACACGCGCGCGAGAGTGAAGTCTCAAGAG 720
 Db 1321 ATGGAATTTAATTTCCCGTTCGCCCAACACGCGCGCGAGAGTGAAGTCTCAAGAG 1380
 QY 721 AGCCGAGAGTCAAGTGTGCAATCGTGGTGGCGGCGCGCTCCCTTTATAGCCGA 780
 Db 1381 AGCCGAGAGTCAAGTGTGCAATCGTGGTGGCGGCGCGCTCCCTTTATAGCCGA 1440
 QY 781 CTGCGCCGAGAGGCAACCGGGTGGGAGGCTGGGAGGGTGGTGGCCATTTT 840
 Db 1441 CTGCGCCGAGAGGCAACCGGGTGGGAGGCTGGGAGGGTGGTGGCCATTTT 1500
 QY 841 TGCTAACCTTAAGTGAAGGGCGTA 867
 Db 1501 TGCTAACCTTAAGTGAAGGGCGTA 1527
 RESULT 10
 ARI61905 LOCUS 2426 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 3 from patent US 6258535.
 ACCESSION ARI61905
 VERSION ARI61905.1 GI:16228915

KEYWORDS	UNKNOWN.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 2426)
AUTHORS	Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE	Mammalian telomerase
JOURNAL	Patent: US 6258535-A 3 10-JUL-2001;
FEATURES	Location/Qualifiers 1..2426
source	/organism="unknown"
BASE COUNT	620 a 575 c 650 g 581 t
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Query Match	97.9% ; Score 848.6; DB 6; Length 2426;
Best Local Similarity	99.4% ; Pred.No.1.4e-234;
Matches 862; Conservative	0; Mismatches 4; Indels 1; Gaps 1.
OY	1 ACCTACTCAGGAGCGCTGAGACACGAGAATCGCTTGAAACC GGAGGCAGAGGTCCAGTGG 60
Db	662 ACCTACTCAGGAGCGCTGAGACACGAGAATCGCTTGAAACC GGAGGCAGAGGTCCAGTGG 720
OY	61 ACCCGAGATCACGCCACATGAGACTCCATCCAGCGTCGGGGGAAGACCAAGACATCGCTGCA 120
Db	721 ACCCGAGATCACGCCACATGAGACTCCATCCAGCGTCGGGGGAAGACCAAGACATCGCTGCA 780
OY	121 AAAAAAAAAAATCGTTACAATTATTTGGTGGATTAATCTCCCTCTTTTACCTCATCAAGACA 180
Db	781 AAAAAAAAAAATCGTTACAATTATTTGGTGGATTAATCTCCCTCTTTTACCTCATCAAGACA 840
OY	181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAACGCCCTTTCTTTCTTAATAAAGGAG 240
Db	841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAACGCCCTTTCTTTCTTAATAAAGGAG 900
OY	241 ATTCACTCCTTAAGATTAT 300
Db	901 ATTCACTCCTTAAGATTAT 960
OY	301 AGGAGAACGCTGAGAGAGCATTTCTAAGGAAAAAGGGGGCAGGGTTGGAATCGGACGCATC 360
Db	961 AGGAGAACGCTGAGAGAGCATTTCTAAGGAAAAAGGGGGCAGGGTTGGAATCGGACGCATC 1020
OY	361 CCACAGAGCCCGAGACAAGATTTCTGCTGTAAGTAGTGTGCTGCGGCAATCTATTTTACAA 420
Db	1021 CCACAGAGCCCGAGACAAGATTTCTGCTGTAAGTAGTGTGCTGCGGCAATCTATTTTACAA 1080
OY	421 AGTTCTCCAAAATAATGTGATGATCAAAATAGAAATTAAGTTATAGTTCTGATAGGCCCTTA 480
Db	1081 AGTTCTCCAAAATAATGTGATGATCAAAATAGAAATTAAGTTATAGTTCTGATAGGCCCTTA 1140
OY	481 AAATCTTCTGTGAATTCATTTTTTAAGTATGTCAGAGTGAACCCGCTGTGCTGTGCAGA 540
Db	1141 AAATCTTCTGTGAATTCATTTTTTAAGTATGTCAGAGTGAACCCGCTGTGCTGTGCAGA 1200
OY	541 GGATGAAAAAAGGCCCTCTGTGATACCTCAAGTTAGTTACCTTTAAAGAAAGTCGGANG 600
Db	1201 GGATGAAAAAAGGCCCTCTGTGATACCTCAAGTTAGTTACCTTTAAAGAAAGTCGGANG 1260
OY	601 TAAAGACGCAAAAGCCTTTCCCGAGAGTGGGAGGGAACAGTCCTTCTCATAGGCCGAA 660
Db	1261 TAAAGACGCAAAAGCCTTTCCCGAGAGTGGGAGGGAACAGTCCTTCTCATAGGCCGAA 1320
OY	661 ATGGAATTTTAATTTCCCGTTCCCGCCCAACGAGCCGCGCGAGAGATGACTCTCAGAG 720
Db	1321 ATGGAATTTTAATTTCCCGTTCCCGCCCAACGAGCCGCGCGAGAGATGACTCTCAGAG 1380
OY	721 AGCGCGGAGAGTCAAGCTTTGGCCAATCCGTGCGGTGCGGCGCGCTCCCTTTATAAGCCGA 780
Db	1381 AGCGCGGAGAGTCAAGCTTTGGCCAATCCGTGCGGTGCGGCGCGCTCCCTTTATAAGCCGA 1440
OY	781 CTCGCCGGCGAGCGCACCGGGGTTGGGAGAGGGTGGGCTCTGGGAAGGGGTGGCCATTTTT 840
Db	1441 CTCGCCGGCGAGCGCACCGGGGTTGGGAGAGGGTGGGCTCTGGGAAGGGGTGGCCATTTTT 1500

QY	841	TGCTTAACCCCTACTGAGAGAAGGGCGTGA	867
Db	1501	TGCTTAACCCCTACTGAGAGAAGGGCGTGA	1527
RESULT 11			
AR081665			
LOCUS	AR081665	981 bp	DNA
DEFINITION	Sequence 2 from patent US 5972605.		linear
ACCSSION	AR081665		PAT 31-AUG-2000
VERSION	AR081665.1	GI:10008391	
KEYWORDS	.		
SOURCE	unknown.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 981)		
AUTHORS	Villepoiteau,B., Feng,J., Andrews,W.H. and Adams,R.R.		
TITLE	Assays for regulators of mammalian telomerase expression		
JOURNAL	Patent: US 5972605-A 2 26-OCT-1999;		
FEATURES	location/Qualifiers		
source	1..981		
	/organism="unknown"		
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ORIGIN			
Query Match	38.5%; Score 334; DB 6; Length 981;		
Best Local Similarity	100.0%; Pred. No. 1.3e-85;		
Matches 334:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	534	CTGCAGAGATGTGAAAAAAGGCCCTCATATACCTCAAGTTAGTTTCACCTTAAAGAAG	593
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QY	594	TGCGAAGTAAACAGCSCAAAGCCTTCCCGGAGTGTCGGAGAGGCGAACCTCCTTCATG	653
Db	61	TGCGAAGTAAAGACSCCAAAGCCTTCCCGGAGTGTCGGAGAGGCGAACCTCCTTCATG	120
QY	654	GCCGGAATGGAACTTTAATTTCCCGTTCGCCCAACAGCCCCCGAGAGAGTAGTC	713
Db	121	GCCGGAATGGAACTTTAATTTCCCGTTCGCCCAACAGCCCCCGAGAGAGTAGTC	180
QY	714	TCACAGAGACCGCGAGAGCTAGCTTGCCCAATMCGTGCGGTTCGGCGCCGCTCCCTTTAT	773
Db	181	TCACAGAGACCGCGAGAGCTAGCTTGCCCAATMCGTGCGGTTCGGCGCCGCTCCCTTTAT	240
QY	774	AAGCCGACTCGCCCGCGCACCGCGGTTCGGAGAGGTGGGCTTGAGAGGGGTGTGGC	833
Db	241	AAGCCGACTCGCCCGCGCACCGCGGTTCGGAGAGGTGGGCTTGAGAGGGGTGTGGC	300
QY	834	CATTTTGTCTAACCCCTAAGCTGAGAAAGGGCGTGA	867
Db	301	CATTTTGTCTAACCCCTAAGCTGAGAAAGGGCGTGA	334
RESULT 12			
AR028774			
LOCUS	AR028774	981 bp	DNA
DEFINITION	Sequence 5 from patent US 5858777.		linear
ACCSSION	AR028774		PAT 29-SEP-1999
VERSION	AR028774.1	GI:5940747	
KEYWORDS	.		
SOURCE	unknown.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 981)		
AUTHORS	Villepoiteau,B., Feng,J., Andrews,W.H. and Adams,R.R.		
TITLE	Methods and reagents for regulating telomere length and telomerase activity		
JOURNAL	Patent: US 5858777-A 5 12-JAN-1999;		
FEATURES	location/Qualifiers		
source	1..981		
	/organism="unknown"		

BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

Query Match 38.4%; Score 333; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.5e-85;
Matches 333: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 120

QY 654 GCCGGAATGGAACCTTAATTTCCCGTTCGCCCAACGAGGAGAGTACTC 713
DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCGCCCAACGAGGAGAGTACTC 180

QY 714 TCACGAGAGCCCGAGAGTCAAGTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGAGCCCGAGAGTCAAGTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGGTTGGGAGGTGGGCTTGGGAAGGGTGTGTC 833
DB 241 AAGCCGACTCGCCCGGCAACGCGGTTGGGAGGTGGGCTTGGGAAGGGTGTGTC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867
DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 13
AX022166

LOCUS AX022166 981 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from Patent EP0953042.
ACCESSION AX022166
VERSION AX022166.1 GI:10045843
KEYWORDS

SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Andrews,M.H., Villeponteau,B., Adams,R.R. and Feng,J.
TITLE Methods and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: EP 0953042-A 5 03-NOV-1999;
GERON CORP (US)

FEATURES
source Location/Qualifiers
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BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

Query Match 38.4%; Score 333; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.5e-85;
Matches 333: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 120

QY 654 GCCGGAATGGAACCTTAATTTCCCGTTCGCCCAACGAGGAGAGTACTC 713
DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCGCCCAACGAGGAGAGTACTC 180

DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCGCCCAACGAGGAGAGTACTC 180

QY 714 TCACGAGAGCCCGAGAGTCAAGTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGAGCCCGAGAGTCAAGTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGGTTGGGAGGTGGGCTTGGGAAGGGTGTGTC 833
DB 241 AAGCCGACTCGCCCGGCAACGCGGTTGGGAGGTGGGCTTGGGAAGGGTGTGTC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867
DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 14
A84591

LOCUS A84591 981 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 1 from Patent WO9845450.
ACCESSION A84591
VERSION A84591.1 GI:6733507
KEYWORDS

SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Atkinson,E.M. and Kealey,J.T.
TITLE PURIFIED TELOMERASE
JOURNAL Patent: WO 9845450-A 1 15-OCT-1998;
GERON CORP (US)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
267..716
/product="HTR"
/note="RNA COMPONENT OF HUMAN TELOMERASE (HTR)"

BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

Query Match 38.3%; Score 332.4; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.7e-85;
Matches 333: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 120

QY 654 GCCGGAATGGAACCTTAATTTCCCGTTCGCCCAACGAGGAGAGTACTC 713
DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCGCCCAACGAGGAGAGTACTC 180

QY 714 TCACGAGAGCCCGAGAGTCAAGTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGAGCCCGAGAGTCAAGTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGGTTGGGAGGTGGGCTTGGGAAGGGTGTGTC 833
DB 241 AAGCCGACTCGCCCGGCAACGCGGTTGGGAGGTGGGCTTGGGAAGGGTGTGTC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867
DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 15
AR063825

LOCUS AR063825 981 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5846723.

ACCESSION AR063825
VERSION AR063825.1 GI:5993133
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 981)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 1 08-DEC-1998;
FEATURES Location/Qualifiers
source 1..981
BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

Query Match 38.3%; Score 332.4; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.7e-85;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTCGAGAGATGAAAAAGCCCTCGATACCTCAAGTTAGTTACCTTAAGAAG 593
|||
Db 1 CTCAGAGGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTACCTTAAGAAG 60

QY 594 TCGAAGTAAGAAGCAAGCCCTTCCCGAGCTGCGAAGGCAACGTCCTTCATG 653
|||
Db 61 TCGAAGTAAGAAGCAAGCCCTTCCCGAGCTGCGAAGGCAACGTCCTTCATG 120

QY 654 GCGGAAATGGAACCTTAATTTCCTGCTCCCAACCAAGCCCGCCGAGAGTACTC 713
|||
Db 121 GCGGAAATGGAACCTTAATTTCCTGCTCCCAACCAAGCCCGCCGAGAGTACTC 180

QY 714 TCACGAGAGCCGCGAGAGTCAGCTTGCCCATCGGTGCGGCGCGCCCTTTAT 773
|||
Db 181 TCACGAGAGCCGCGAGAGTCAGCTTGCCCATCGGTGCGGCGCGCCCTTTAT 240

QY 774 AAGCCGACTGCGCGGAGCGCACCGGGTTGCGGAGGGTGGCCGGAAGGGTGGGC 833
|||
Db 241 AAGCCGACTGCGCGGAGCGCACCGGGTTGCGGAGGGTGGCCGGAAGGGTGGGC 300

QY 834 CATTGTTGCTAACCTTAAGTGAAGGCGTA 867
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Db 301 CATTGTTGCTAACCTTAAGTGAAGGCGTA 334

Search completed: January 25, 2003, 15:53:38
Job time : 3242 secs

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OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:41:55 : Search time 303 Seconds
(without alignments)
6443.837 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867

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Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867	100.0	867	20	AAZ07250
2	867	100.0	1765	20	AAZ07247
3	848.6	97.9	2426	19	AAV22994
4	834.6	96.3	2425	17	AAI10283
5	834.6	96.3	2425	17	AAI10283
6	334	38.5	981	19	AAV41194
7	334	38.5	981	19	AAV19481
8	333	38.4	980	22	AA509471
9	333	38.4	981	24	AAZ24234

10	332.4	38.3	981	18	AAI89242	Clone containing h
11	332.4	38.3	981	19	AAV63644	Human telomerase R
12	332.4	38.3	981	20	AAZ23626	Human clone 28-1 c
13	332.4	38.3	981	21	AAI37564	Human telomerase n
14	332.4	38.3	981	23	AAI51442	PcLi fragment cont
15	176	20.3	176	20	AAZ07323	Human telomerase R
16	176	20.3	176	20	AAZ07251	Human telomerase R
17	155	17.9	680	18	AAI58803	Human telomerase e
18	106	12.2	15650	22	ABAI5903	Human nervous syst
19	106	12.2	15650	22	ABAI5364	Human nervous syst
20	106	12.2	42738	22	AAI68992	Human immune/haema
21	104.8	12.1	26928	22	ABAI82620	Human HBW gene reg
22	104.8	12.1	26928	24	ABK22779	Human high bone ma
23	104.4	12.0	20245	22	AAK72318	Human immune/haema
24	104.4	12.0	20245	22	ABK69845	Human secreted pro
25	104.4	12.0	84607	20	AAI90847	Human PKAP genoml
26	104.4	12.0	220895	24	ABK84798	Human cDNA differe
27	104	12.0	32134	22	ABAI07813	Human cDNA differe
28	104	12.0	32134	22	AAI03615	Human reproductive
29	104	12.0	32191	22	ABAI07814	Human ovarian and
30	104	12.0	32191	22	AAI03615	Human reproductive
31	102.8	11.9	15810	24	AAI68995	Human ationatriur
32	102.8	11.9	22465	22	AAK86932	Human immune/haema
33	102.8	11.9	44100	21	ABN97975	Human retroviral s
34	102.8	11.9	56093	24	ABL61744	Colon adenocarcino
35	102.6	11.8	5121	22	AAK83937	Human immune/haema
36	102.6	11.8	31853	22	AAI98993	Human excretory re
37	102.6	11.8	31853	22	AAI63343	Human kidney relat
38	102	11.8	18564	22	AAK65368	Human immune/haema
39	101.8	11.7	23544	22	AAI05829	Human reproductive
40	101.8	11.7	23544	23	ABL98393	Human testicular a
41	101.6	11.7	421	23	ABV17393	Human prostate exp
42	101.6	11.7	480	23	ABV47188	Human prostate exp
43	101.6	11.7	139389	24	ABK84795	Human cDNA differe
44	101.4	11.7	177	21	AAI12382	Human secreted pro
45	101.2	11.7	405	23	ABV49060	Human prostate exp

ALIGNMENTS

RESULT 1	
AAZ07250	AAZ07250 standard; DNA; 867 BP.
ID	AAZ07250
AC	AAZ07250;
XX	
DT	22-OCT-1999 (first entry)
DE	Human telomerase RNA gene (hTR) 5' flanking region.
XX	
KW	Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KW	gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
OS	Homo sapiens.
XX	
PN	MO9938964-A2.
PD	05-AUG-1999.
XX	
PF	29-JAN-1999; 99WO-GB00308.
XX	
PR	29-JAN-1998; 98GB-0001902.
XX	
PA	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX	
PI	Keith WN;
XX	
DR	WPI: 1999-479183/40.
XX	
PT	Mouse and human telomerase RNA gene promoters, useful for tumor
PT	specific gene therapy
XX	

PS Claim 3; Fig 4a; 109pp; English.
XX
CC The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy
CC of cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These
CC substances, e.g. antisense oligonucleotides, transcription factors,
CC peptide nucleic acids and factors that disrupt signal transduction, are
CC useful for cancer therapy. In particular, gene therapy vectors
CC (especially pG62-codapp) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a product, e.g. gancyclovir, so that
CC neoplasia can be controlled or treated. Direct down-regulation of
CC telomerase RNA gene through manipulation of transcription factors may be
CC effective anticancer therapy and the cloning of the hTR gene promoter
CC allows the analysis of therapeutic molecules which modulate hTR promoter
CC activity. The present sequence represents a human TR gene (hTR)
CC 5' flanking sequence.
XX

Sequence 867 BP; 237 A; 209 C; 221 G; 200 T; 0 other;

Query Match 100.0%; Score 867; DB 20; Length 867;
Best Local Similarity 100.0%; Pred. No. 3.7e-268;

Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGGCTGAGACACAGAGATCGCTTGAACCGGGAGCAGAGCTGCAGTG 60
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QY 61 AGCCGAGATCAGCCACTGACATCCAGCCCTGGGCGAAGAGAGAGAGCTCCGCTCA 120
DB 61 AGCCGAGATCAGCCACTGACATCCAGCCCTGGGCGAAGAGAGAGAGCTCCGCTCA 120
QY 121 AAAAAAATCGTTCAATTTATGTTGATTAATCTCCCTTTTTCATCATCAAGACA 180
DB 121 AAAAAAATCGTTCAATTTATGTTGATTAATCTCCCTTTTTCATCATCAAGACA 180
QY 181 CAGCACTACTTTAAAGCAAGTCATGATTGAAGCCCTTTCTTCTTAATAAGAGAG 240
DB 181 CAGCACTACTTTAAAGCAAGTCATGATTGAAGCCCTTTCTTCTTAATAAGAGAG 240
QY 241 ATTCACTCCTTAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 ATTCACTCCTTAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 AGGAGAAGCTGGAGAGGATTTCTAAGAAAAAGGGGAGGGTTGGAGCTCGAGCATC 360
DB 301 AGGAGAAGCTGGAGAGGATTTCTAAGAAAAAGGGGAGGGTTGGAGCTCGAGCATC 360
QY 361 CCACGTAGAGCCGAGACAAATTTGCTGTAGTACAGTCTCCCTGGGAATCTATTTTCACA 420
DB 361 CCACGTAGAGCCGAGACAAATTTGCTGTAGTACAGTCTCCCTGGGAATCTATTTTCACA 420
QY 421 AGTTCTCCAAAAATGTGATCAAACTAGGAATTAAGTATGATGATGATGATGATGAT 480
DB 421 AGTTCTCCAAAAATGTGATCAAACTAGGAATTAAGTATGATGATGATGATGATGAT 480
QY 481 AATCTTCTGTAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGTGCTGTCAGACA 540
DB 481 AATCTTCTGTAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGTGCTGTCAGACA 540
QY 541 GGATAGAAAAAGGCGCTGTGATCAAGTTAGTTTACCTTTAAAGAGGTGGAG 600
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DB 601 TAAAGACGCAAGCCCTTCCGAGAGTGGGGAAGGCAAGCTCCCTCATGAGCGCGGA 660

QY 661 ATGGAACCTTAATTTCCCTCCCAACAGACCCCGGAGAGAGTACTCTACAGAG 720
DB 661 ATGGAACCTTAATTTCCCTCCCAACAGACCCCGGAGAGAGTACTCTACAGAG 720
QY 721 AGCCGAGAGTCAAGCTTGCCCAATCCGTGCGGTGCGGCGCTCCCTTATTAAGCCGA 780
DB 721 AGCCGAGAGTCAAGCTTGCCCAATCCGTGCGGTGCGGCGCTCCCTTATTAAGCCGA 780
QY 781 CTGCGCCGCGAGCGACCGGGTTGCGGAGCGTGGCGGAGAGGTGGTGGCCATT 840
DB 781 CTGCGCCGCGAGCGACCGGGTTGCGGAGCGTGGCGGAGAGGTGGTGGCCATT 840
QY 841 TGCTAACCTTAAGTGAAGGCGCTGA 867
DB 841 TGCTAACCTTAAGTGAAGGCGCTGA 867

RESULT 2

AA07247 standard; DNA; 1765 BP.

AA07247;

22-OCT-1999 (first entry)

Human telomerase RNA (hTR) gene sequence.

Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KW gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

Homo sapiens.

W09338964-A2.

05-AUG-1999.

29-JAN-1999; 99WO-GB00308.

29-JAN-1998; 98GB-0001902.

(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

Kelth WN;

WPI: 1999-479183/40.

Mouse and human telomerase RNA gene promoters, useful for tumor
PT specific gene therapy

PS Disclosure; Fig 1; 109pp; English.

The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy
CC of cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These
CC substances, e.g. antisense oligonucleotides, transcription factors,
CC peptide nucleic acids and factors that disrupt signal transduction, are
CC useful for cancer therapy. In particular, gene therapy vectors
CC (especially pG62-codapp) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a product, e.g. gancyclovir, so that
CC neoplasia can be controlled or treated. Direct down-regulation of
CC telomerase RNA gene through manipulation of transcription factors may be
CC effective anticancer therapy and the cloning of the hTR gene promoter
CC allows the analysis of therapeutic molecules which modulate hTR promoter
CC activity. The present sequence represents a human TR (hTR) gene sequence.
XX
SQ Sequence 1765 BP; 404 A; 458 C; 480 G; 423 T; 0 other;


```

Query Match          100.0%; Score 867; DB 20; Length 1765;
Best Local Similarity 100.0%; Pred. No. 5,5e-268;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 AGCCGAGATCAGCGCCACTGACATCCATCCAGCCCTGGCGAAAGACAACCCCGCTCA 120
DB 61 AGCCGAGATCAGCGCCACTGACATCCATCCAGCCCTGGCGAAAGACAACCCCGCTCA 120
OY 121 AAAAAAAAAATGTTACAAATTTATGGTGATTACTCCCTCTTTTACCTCATCAAGACA 180
DB 121 AAAAAAAAAATGTTACAAATTTATGGTGATTACTCCCTCTTTTACCTCATCAAGACA 180
OY 181 CAGCACTACTTTAAGCAAAAGTCATGATTGAACGCCCTTTCTTCTTAATAAAGGAG 240
DB 181 CAGCACTACTTTAAGCAAAAGTCATGATTGAACGCCCTTTCTTCTTAATAAAGGAG 240
OY 241 ATTCACTCTTAAAGTAAATTAATGATGATTAACCTGATTAACCCATCCCTGCTCA 300
DB 241 ATTCACTCTTAAAGTAAATTAATGATGATTAACCCATCCCTGCTGCTCA 300
OY 301 AGGAGAACTGGAGAGAGCATTTCTAAGAGAAAAAGGGCAGGTTGGAACTCGAGCATC 360
DB 301 AGGAGAACTGGAGAGAGCATTTCTAAGAGAAAAAGGGCAGGTTGGAACTCGAGCATC 360
OY 361 CCACGTGAGCCGAGACAAAGTTCTGCTGATGATGATGCTGCTGGGAATGATTTTCACA 420
DB 361 CCACGTGAGCCGAGACAAAGTTCTGCTGATGATGATGCTGCTGGGAATGATTTTCACA 420
OY 421 ACCTTCCCAAAAAATGTGATCAAAACTAGGAATTAAGTCTCTGCTCTAGAGCCCTA 480
DB 421 ACCTTCCCAAAAAATGTGATCAAAACTAGGAATTAAGTCTCTGCTCTAGAGCCCTA 480
OY 481 AATCTTCTCTGTAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGCTGCTCACA 540
DB 481 AATCTTCTCTGTAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGCTGCTCACA 540
OY 541 GGATAGAAAAAGGCCCTGTGATACCTCAAGTATGATTTACCTTTAAAGAGGTCGGAAG 600
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OY 601 TAAAGACGCAAAAGCCTTTCCGAGAGTGGGAAAGGCAACGTCCTTCATGCGCGGAA 660
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OY 661 ATGGAACCTTAATTTCCGCTCCGCCCAACAGCCCGCCGAGAGAGTACTCTACGAG 720
DB 661 ATGGAACCTTAATTTCCGCTCCGCCCAACAGCCCGCCGAGAGAGTACTCTACGAG 720
OY 721 AGCCGAGAGTACGCTTGCCCAATCCGTCGGCGTCCGCGCTCTTTATTAACCGCA 780
DB 721 AGCCGAGAGTACGCTTGCCCAATCCGTCGGCGTCCGCGCTCTTTATTAACCGCA 780
OY 781 CTGCGCCGCGACGCGACCGCGGTTGGGAGGTCGGGCTTGAGAGGGTGGTGGCCATTTT 840
DB 781 CTGCGCCGCGACGCGACCGCGGTTGGGAGGTCGGGCTTGAGAGGGTGGTGGCCATTTT 840
OY 841 TGTCTAACCCTTAACGTAGAAGGCGCTA 867
DB 841 TGTCTAACCCTTAACGTAGAAGGCGCTA 867

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RESULT 3
AAV22994
ID AAV22994 standard; DNA; 2426 BP.
XX
AC AAV22994:
XX
DT 30-JUL-1998 (first entry)
XX

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DE DNA containing human telomerase RNA component gene sequences.
XX
KW Human; telomerase RNA component gene sequence;
KW Ribonucleoprotein enzyme; cancer cell; telomerase activity;
KW reporter construct; transcription regulatory region;
KW prophylaxis; therapy; telomerase-related condition;
KW chromatin position effect; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT TATA_signal 1438..1444
FT /tag= a
FT misc_feature 1238..1259
FT /tag= b
FT misc_feature 1406..1414
FT /note= "PSE consensus sequence"
FT /tag= c
FT CAAT_signal 1399..1406
FT /note= "PSE consensus sequence"
FT /tag= d
FT misc_feature 1354..1359
FT /tag= e
FT misc_feature 1234..1245
FT /note= "SPl consensus sequence"
FT /tag= f
FT /note= "beta-interferon response element"
XX
PN W09811207-A2.
XX
PD 19-MAR-1998.
XX
PR 16-SEP-1997; 97WO-US16450.
XX
PR 16-SEP-1996; 96US-0714482.
XX
PA (GERO-) GERON CORP.
XX
PI Harley C, Villeponteau B;
XX
DR WPI; 1998-207376/18.
XX
PT Human telomerase reporter constructs - useful in assays for
PT regulators of mammalian telomerase expression
XX
PS Claim 6; Pages 27-28; 59pp; English.
XX
CC The present sequence contains human telomerase RNA component gene
CC sequences. Telomerase is a ribonucleoprotein enzyme that synthesizes
CC one strand of the telomeric DNA using as a template a sequence contained
CC within the RNA component of the enzyme. Most cancer cells express high
CC levels of telomerase activity, while in normal somatic human cells,
CC telomerase is not detected. The specification describes the production
CC of a telomerase reporter construct which comprises a recombinant
CC polynucleotide having a transcription regulatory region of a telomerase
CC gene operably linked to a nucleotide sequence encoding a reporter
CC polynucleotide heterologous to the transcription regulatory region.
CC Expression of the reporter polynucleotide is detectable. The telomerase
CC reporter construct is used in screening assays for determining modulators
CC of transcription. The modulators can be used for prophylaxis or therapy
CC of telomerase-related conditions. The reporter construct which has a
CC selectable drug marker can be used to generate position effect reporter
CC cells which can be used to determine whether a test agent inhibits
CC chromatin position effect. Tagged RNA component constructs can be used
CC to determine whether an agent modulates association between a mammalian
CC RNA telomerase component and a mammalian telomerase.
XX
SQ Sequence 2426 BP; 620 A; 575 C; 650 G; 581 T; 0 other;

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Query Match          97.9%; Score 848.6; DB 19; Length 2426;
Best Local Similarity 99.4%; Pred. No. 5,5e-262;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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 DB 662 AGCTACTCAGAGGCTGAGACACAGAGATCGTTGAACCCGGGAGGCGAGAGTTCAGTGG 720
 QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGGCGAAGAGACAGACTCCGTCTCA 120
 DB 721 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGGCGAAGAGAGACTCCGTCTCA 780
 QY 121 AAAAAAAAAATCGTTACATTTATGGGATTAATCTCCCTCTTTTACCCATCAAGACACA 180
 DB 781 AAAAAAAAAATCGTTACATTTATGGGATTAATCTCCCTCTTTTACCCATCAAGACACA 840
 QY 181 CAGCACTACTTTAAAGCAAGTCATGATTGAAGCCCTTTCTTCTTAATAAAGGAG 240
 DB 841 CAGCACTACTTTAAAGCAAGTCATGATTGAAGCCCTTTCTTCTTAATAAAGGAG 900
 QY 241 ATTCACTCCTTAAGATTAATATGTAGTACTTACACTTATTAAAGCCATCCTCTCTCA 300
 DB 901 ATTCACTCCTTAAGATTAATATGTAGTACTTACACTTATTAAAGCCATCCTCTCTCA 960
 QY 301 AGGAGAGCTGGAGAGGCAATTCCTTAAGCAAAAAGGGGAGGGTGGAACTCGAGCGCATC 360
 DB 961 AGGAGAGCTGGAGAGGCAATTCCTTAAGCAAAAAGGGGAGGGTGGAACTCGAGCGCATC 1020
 QY 361 CCACTGAGCGGAGACAAATTCCTGTAGTCACTGCTGCTGGGAATCATTTTCACAA 420
 DB 1021 CCACTGAGCGGAGACAAATTCCTGTAGTCACTGCTGCTGGGAATCATTTTCACAA 1080
 QY 421 AGTTCTCCAAAAATGTGATGATCAAAACTAGGAATTAAGTCTGTCTGTAGAGCCCTA 480
 DB 1081 AGTTCTCCAAAAATGTGATGATCAAAACTAGGAATTAAGTCTGTCTGTAGAGCCCTA 1140
 QY 481 AATCTTCTGTGAATTCATTTTAAAGGATGAGAGTGAACCCGGCTGGTCCGACAGA 540
 DB 1141 AATCTTCTGTGAATTCATTTTAAAGGATGAGAGTGAACCCGGCTGGTCCGACAGA 1200
 QY 541 GGATAGAAAAAGGCGCTGTGATCTCAAGTTAGTTTCACTTTAAAGAGGTCCGGAAG 600
 DB 1201 GGATAGAAAAAGGCGCTGTGATCTCAAGTTAGTTTCACTTTAAAGAGGTCCGGAAG 1260
 QY 601 TTAAGAGCGAAGGCTTCCCGGAGCTGGGGAAGGCAAGTCTTCCATGAGCCGGA 660
 DB 1261 TTAAGAGCGAAGGCTTCCCGGAGCTGGGGAAGGCAAGTCTTCCATGAGCCGGA 1320
 QY 661 ATGGAATTTAATTTCCCTTCCCGGAGCGGCGGCGGAGAGTCACTCTGACGAG 720
 DB 1321 ATGGAATTTAATTTCCCTTCCCGGAGCGGCGGCGGAGAGTCACTCTGACGAG 1380
 QY 721 AGCCGAGAGTCACTGAGTGGCAATCCGTGCGGTGGCGGCTCTTTTAAAGCCGA 780
 DB 1381 AGCCGAGAGTCACTGAGTGGCAATCCGTGCGGTGGCGGCTCTTTTAAAGCCGA 1440
 QY 781 CTCGCGCGGAGGCGGAGGCTGGGAGGAGGCTGGGAGGAGGAGTGGTGGCATTTT 840
 DB 1441 CTCGCGCGGAGGCGGAGGCTGGGAGGAGGCTGGGAGGAGGAGTGGTGGCATTTT 1500
 QY 841 TGTCTAAACCTACTAGAGAGGCGCTA 867
 DB 1501 TGTCTAAACCTACTAGAGAGGCGCTA 1527

RESULT 4
 AAT10283 standard; DNA: 2425 BP.

XX AAT10283;
 XX AAT10283;

DT 09-SEP-1996 (first entry)

XX Gene for RNA component of human telomerase.

KW RNA component; human; telomerase; lung fibroblast; cell line WI-38;

recombinant production; synthesis; mutant; detection; mammalian;

KW recombinant production; synthesis; mutant; detection; mammalian;

KW Identification; modulating agent; neoplastic condition; gene;
 KW transcriptional regulatory sequence; gene therapy; disease; ss.
 OS Homo sapiens.
 PN WO9601835-A1.
 PD 25-JAN-1996.
 PE 06-JUL-1995; 95WO-US08530.
 PR 07-JUN-1995; 95US-0482115.
 PR 07-JUL-1994; 94US-0272102.
 PR 27-OCT-1994; 94US-0330123.
 PR 07-JUN-1995; 95US-0472802.
 PA (GERO-) GERON CORP.
 PI Andrews WH, Feng J, Funk W, Villeponteau B;
 PI WPI: 1996-097581/10.
 PS RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents
 PT Claim 14; Pages 97-98; 114pp; English.
 CC The present sequence is the gene for the RNA component of human
 CC telomerase (RCHT), which was derived from a genomic DNA library
 CC obtd. from the human lung fibroblast cell line WI-38. The gene
 CC and the RCHT can be used in the recombinant prodn. of an active
 CC telomerase mol., capable of adding sequences to chromosomal DNA
 CC telomeres, and in the synthesis of mutant sequences for the
 CC detection of mutant mammalian telomerase RNA component
 CC polynucleotides. The RCHT may also be used in the identification
 CC of telomerase modulating agents, and in the detection of
 CC telomerase related, or neoplastic conditions in a patient.
 CC Polynucleotides of at least 25 consecutive nucleotides identical,
 CC or complementary to the RCHT sequence linked to heterologous
 CC transcriptional regulatory sequences, can be used for the gene
 CC therapy of human diseases.
 CC XX
 SQ Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 other;
 Query Match 96.3%; Score 834.6; DB 17; Length 2425;
 Best Local Similarity 99.0%; Pred. No. 1.7e-257;
 Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;
 QY 1 AGCTACTCAGAGGCTGAGACACAGAGATCGTTGAACCCGGGAGGCGAGAGTTCAGTGG 60
 DB 662 AGCTACTCAGAGGCTGAGACACAGAGATCGTTGAACCCGGGAGGCGAGAGTTCAGTGG 720
 QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGGCGAAGAGACAGACTCCGTCTCA 120
 DB 721 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGGCGAAGAGAGACTCCGTCTCA 780
 QY 121 AAAAAAAAAATCGTTACATTTATGGGATTAATCTCCCTCTTTTACCCATCAAGACACA 180
 DB 781 AAAAAAAAAATCGTTACATTTATGGGATTAATCTCCCTCTTTTACCCATCAAGACACA 840
 QY 181 CAGCACTACTTTAAAGCAAGTCATGATTGAAGCCCTTTCTTCTTAATAAAGGAG 240
 DB 841 CAGCACTACTTTAAAGCAAGTCATGATTGAAGCCCTTTCTTCTTAATAAAGGAG 900
 QY 241 ATTCACTCCTTAAGATTAATATGTAGTACTTACACTTATTAAAGCCATCCTCTCTCA 300
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 QY 301 AGGAGAGCTGGAGAGGCAATTCCTTAAGCAAAAAGGGGAGGGTGGAACTCGAGCGCATC 360
 DB 961 AGGAGAGCTGGAGAGGCAATTCCTTAAGCAAAAAGGGGAGGGTGGAACTCGAGCGCATC 1020
 QY 361 CCACTGAGCGGAGACAAATTCCTGTAGTCACTGCTGCTGGGAATCATTTTCACAA 420

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|||||
Db 1021 CCACGTGAGCCGAGCAGCAATCTGCTGTACTGCTGCTGCTGCAATCTATTTCACAA 1080
Oy 421 AGTTCCTCAAAAATGATGATCAAAACAGAAATAGTCTGTGCTTGGCCCTA 480
Db 1081 AGTTCTCCAAAATGATGATCAAAACAGAAATAGTCTGTGCTTGGCCCTA 1140
Oy 481 AATCTTCTGTGATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGCTGCAGA 540
Db 1141 AATCTTCTGTGATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGCTGCAGA 1200
Oy 541 GGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAGTCGGAAG 600
Db 1201 GGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAGTCGGAAG 1260
Oy 601 TAAAGACGAAAGCCTTCCCGGACGTCGGGAAGGCAAGCTCTCTATGGCCGAA 660
Db 1261 TAAAGACGAAAGCCTTCCCGGACGTCGGGAAGGCAAGCTCTCTATGGCCGAA 1320
Oy 661 ATGAACTTTAATTTCCCGTTCCCGCAACACGCGCCGAGAGAGTAGTCTCACGAG 720
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Oy 721 AGCCGCGAGAGTAGTCTTGCCCAATCCGTGCGGTGCGGCGCTCTTTATAAGCCGA 780
Db 1381 AGCCGCGAGAGTAGTCTTGCCCAATCCGTGCGGTGCGGCGCTCTTTATAAGCCGA 1440
Oy 781 CTGCGCCGCGAGCGACCGGGGTTGC---GGAGGCTGGGCTGGAGAGGTTGGGCCAT 836
Db 1441 CTGCGCCGCGAGCGACCGGGGTTGC---GGAGGCTGGGCTGGAGAGGTTGGGCCAT 1500
Oy 837 TTTTGTCTTAACCTTAACCTGAAGAGGCGCTA 867
Db 1501 TTTTGTCTTAACCTTAACCTGAAGAGGCGCTA 1531

RESULT 5
AAT11027
ID AAT11027 standard: DNA: 2425 BP.
XX
AC AAT11027:
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the human telomerase RNA component.
XX
KW Telomerase; mammal; antisense; tripleplex forming oligonucleotide;
KW plasmid; probe; primer; ribozyme; ss.
XX
OS Homo sapiens.
XX
PN W09601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95MO-US086620.
XX
PR 07-JUN-1995; 95US-0485778.
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 13-FEB-1995; 95US-0387524.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Avillion AA, Feng J, Funk W, Greider C;
PI Morhunda MA, Villeponteau B;
XX
DR WPI: 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in
PT studying cell senescence and immortalisation
XX
```

```
PS Claim 37: Figure 1: 85bp: English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially
CC from mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the
CC telomerase: probes and primers can be used in detection: vectors and
CC host cells transformed with the isolated telomerase genes can be
CC used for production of telomerases: RNA and DNA ribozymes and triplex
CC forming oligonucleotides directed against the telomerase genes can
CC be used therapeutically as can plasmids. A mouse which lacks the
CC telomerase gene (also claimed) can be used for study of telomere
CC regulation in vivo, and the role it plays in immortalisation. This
CC DNA sequence encodes the human telomerase RNA component.
XX
SQ Sequence 2425 BP: 622 A; 572 C; 650 G; 581 T: 0 other:
Query Match 96.3%; Score 834.6; DB 17; Length 2425;
Best Local Similarity 99.0%; Pred. No. 1.7e-257;
Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;
Oy 1 AGCTACGAGGAGCGTAGACAGAGAAATCGTTGAACCGGGAGGACAGAGTTGGAGTG 60
Db 662 AGCTACGAGGAGCGTAGACAGAGAAATCGTTGAACCGGGAG-6CAGAGTTGCAAGTG 720
Oy 61 AGCCGAGATCACGCCACTAGACTCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
Db 721 AGCCGAGATCACGCCACTAGACTCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780
Oy 121 AAAAAAAAAATCGTTACATTTATGCTGATTACTGCCCTCTTTTAACTCATCAAGACA 180
Db 781 AAAAAAAAAATCGTTACATTTATGCTGATTACTGCCCTCTTTTAACTCATCAAGACA 840
Oy 181 CAGCAGTACTTTAAGAAAGTCAATGATGAAGCGCTTCTCTTAATAAAGGAG 240
Db 841 CAGCAGTACTTTAAGAAAGTCAATGATGAAGCGCTTCTCTTAATAAAGGAG 900
Oy 241 ATTCACTCTTAAGATTAATATATAGTAGTACACTTGAATTAAGCCATCTCTGCTCA 300
Db 901 ATTCACTCTTAAGATTAATATATAGTAGTACACTTGAATTAAGCCATCTCTGCTCA 960
Oy 301 AGGAGAAAGCTGGAGAAAGCATTTCTAAGGAAAAAGGGCAGGTTGGAACTCGGACCATC 360
Db 961 AGGAGAAAGCTGGAGAAAGCATTTCTAAGGAAAAAGGGCAGGTTGGAACTCGGACCATC 1020
Oy 361 CCACTGAGCCGAGACAAAGATTCGCTAGTACAGTGTGCTGGGGAATCATTTTACAA 420
Db 1021 CCACTGAGCCGAGACAAAGATTCGCTAGTACAGTGTGCTGGGGAATCATTTTACAA 1080
Oy 421 AGTTCTCCAAAATGATGATCAAAACAGAAATAGTCTGTGCTTAGGCCCTA 480
Db 1081 AGTTCTCCAAAATGATGATCAAAACAGAAATAGTCTGTGCTTAGGCCCTA 1140
Oy 481 AATCTTCTGTGATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGCTGCAGA 540
Db 1141 AATCTTCTGTGATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGCTGCAGA 1200
Oy 541 GGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAGTGGGAAG 600
Db 1201 GGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAGTGGGAAG 1260
Oy 601 TAAAGACGAAAGCCTTCCCGGACGTCGGAAGGCAAGCTCTCTCATGGCCGAA 660
Db 1261 TAAAGACGAAAGCCTTCCCGGACGTCGGAAGGCAAGCTCTCTCATGGCCGAA 1320
Oy 661 ATGAACTTTAATTTCCCGTTCCCGCAACACGCGCCGAGAGAGTAGTCTCACGAG 720
Db 1321 ATGAACTTTAATTTCCCGTTCCCGCAACACGCGCCGAGAGAGTAGTCTCACGAG 1380
Oy 721 AGCCGCGAGAGTAGTCTTGCCCAATCCGTGCGGTGCGGCGCTCTTTATAAGCCGA 780
Db 1381 AGCCGCGAGAGTAGTCTTGCCCAATCCGTGCGGTGCGGCGCTCTTTATAAGCCGA 1440
Oy 781 CTGCGCCGCGAGCGACCGGGTTC---GGAGGCTGGGCTGGAGAGGTTGGGCCAT 836
```

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|||||
Db 1441 CTCGCCGCGAGCGACCGGTTGCGAGGAGGAGGTGGCGCTGCGAGGCGTGTGCCCAT 1500
OY 837 TTTTGTCTAACCTACTGAGAGGCGTA 867
Db 1501 TTTTGTCTAACCTACTGAGAGGCGTA 1531

RESULT 6
AAV41194
ID AAV41194 standard; DNA; 981 BP.
XX
AC AAV41194:
DT 08-OCT-1998 (first entry)
XX
DE PstI fragment containing RNA component of human telomerase (hTR).
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FH misc_feature 266..716
FT /tag= a
FT /note= "RNA component of human telomerase (hTR)"
FT misc_feature 311..320
FT /tag= b
FT /note= "template region of hTR"
XX
PN MO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
PI
XX
DR WPI: 1998-377670/32.
XX
PT New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Disclosure; Page 53; 80pp; English.
XX
CC This represents a pstI fragment containing the RNA component of human
CC telomerase (hTR). The invention provides antisense oligonucleotides
CC (AAV41169 to AAV41181) to hTR. These antisense oligonucleotides
CC specifically hybridise to a nucleotide sequence within an accessible
CC region of the hTR, but that does not hybridise to a sequence within the
CC template region of hTR. These oligonucleotides may specifically be used
CC for detection of an RNA component of human telomerase in a sample. This
CC is useful for diagnosing cancer (especially neuroblastoma, bladder, colon
CC and prostate cancer), and providing prognosis for a cancer patient. The
CC inhibitory oligonucleotides can inhibit the telomerase activity level in
CC a cell by interfering with transcription of the RNA component, decreasing
CC the half-life of the telomerase RNA component transcript, inhibiting
CC assembly of the RNA component into the telomerase holoenzyme, or
CC inhibiting the polymerase activity of telomerase. These antisense
CC oligonucleotides can be used for inhibiting telomerase activity in both
CC cultured cells and in cells in vivo. They can be used in therapeutics for
CC treating or preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in anti-
```

```
CC inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;
Query Match 38.5%; Score 334; DB 19; Length 981;
Best Local Similarity 100.0%; Pred. No. 1,1e-96;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 534 CTCGAGAGCATGAAAAAAGCCCTCTGATACCTCAAGTTAGTTACCTTAAAGAAG 593
Db 1 CTCGAGAGCATGAAAAAAGCCCTCTGATACCTCAAGTTAGTTACCTTAAAGAAG 60
OY 594 TCGGAAGTAAGACGCAAAAGCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 653
Db 61 TCGGAAGTAAGACGCAAAAGCTTTCCCGAGCTGGGGAAGGCAACGTCCTTCATG 120
OY 654 GCCGGAATGGAACTTTAATTTCCCGTTCCCCCAACCAAGCCCGCCGAGAGTGACTC 713
Db 121 GCCGGAATGGAACTTTAATTTCCCGTTCCCCCAACCAAGCCCGCCGAGAGTGACTC 180
OY 714 TCACGAGAGCCCGGAGAGTCAGCTTGCCCAATCCGTGCGGTGGCGCGCTCCCTTAT 773
Db 181 TCACGAGAGCCCGGAGAGTCAGCTTGCCCAATCCGTGCGGTGGCGCGCTCCCTTAT 240
OY 774 AACCCGACTGCCCGGAGCGCAACCGGTTGGGAGAGGTGGGCTGGGAGGGTGGGC 833
Db 241 AACCCGACTGCCCGGAGCGCAACCGGTTGGGAGAGGTGGGCTGGGAGGGTGGGC 300
OY 834 CATTTTGTCTAACCTACTGAGAGGCGTA 867
Db 301 CATTTTGTCTAACCTACTGAGAGGCGTA 334

RESULT 7
AAV19481
ID AAV19481 standard; cDNA; 981 BP.
XX
AC AAV19481:
XX
DT 28-AUG-1998 (first entry)
XX
DE Human telomerase hTR gene.
XX
KW Telomerase; hTR gene; TPC2; TPC3; telomere length; human; cancer;
KW gene therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH unsure 21
FT /tag= a
FT mRNA 266..715
FT /tag= b
XX
PN MO9811204-A1.
XX
PD 19-MAR-1998.
XX
PF 13-SEP-1996; 96WO-US14679.
XX
PR 13-SEP-1996; 96WO-US14679.
XX
PA (GERO-) GERON CORP.
XX
PI Adams RR, Andrews WH, Feng J, Villeponteau B;
PI
XX
DR WPI: 1998-207373/18.
XX
PT Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
PT telomerase activity
XX
PS Disclosure; Fig 9A-B; 86pp; English.
```

XX This nucleotide sequence comprises an approximately 1 kb psi
 CC restriction fragment of plasmid pGRN33 that includes the human
 CC telomerase hTR gene. hTR3 mRNA levels correlate with telomerase
 CC activity levels in a variety of mortal and immortal cell lines.
 CC In methods of the invention, measurements of telomere length,
 CC telomerase activity or hTR levels can be used to identify immortal
 CC cells, such as cancer cells, and to evaluate the proliferative
 CC capacity of the cell. Gene therapy vectors encode useful nucleic
 CC acids such as hTR, or antisense nucleic acids or ribozymes that
 CC target TERC, TERC3 (see AAV19479-80) and/or hTR gene products.

XX Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;

Query Match 38.5%; Score 334; DB 19; Length 981;

Best Local Similarity 100.0%; Pred. No. 1,1e-96;

Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 CTGCAGAGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 593
 DB 1 CTGCAGAGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 60
 QY 594 TCGGAAGTAAAGACGCAAGCCTTCCCGAGCTGGCGAAGGCAACGTCCTTCATG 653
 DB 61 TCGGAAGTAAAGACGCAAGCCTTCCCGAGCTGGCGAAGGCAACGTCCTTCATG 120
 QY 654 GCCGAAATGGAATTTATTTCCGTCCTCCCAACAGCCCGCGAGAGAGTACTC 713
 DB 121 GCCGAAATGGAATTTATTTCCGTCCTCCCAACAGCCCGCGAGAGTACTC 180
 QY 714 TCACGAGAGCCGCGAGATCAGTCCGCAATCCGTGCGGTGGCGGCGCTCTTAT 773
 DB 181 TCACGAGAGCCGCGAGATCAGTCCGCAATCCGTGCGGTGGCGGCGCTCTTAT 240
 QY 774 AACCGACTCGCCGCGAGCGCAACGCGGTTGCGGAGGTTGGGCTGGAGGGTGGTGGC 833
 DB 241 AACCGACTCGCCGCGAGCGCAACGCGGTTGCGGAGGTTGGGCTGGAGGGTGGTGGC 300
 QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGTA 867
 DB 301 CATTTTGTCTAACCTTAAGTGAAGGCGTA 334

RESULT 8
 AAS09471
 ID AAS09471 standard; DNA; 980 BP.

XX AAS09471;

XX 24-OCT-2001 (first entry)

XX Human DNA containing the RNA component of telomerase.

XX Human; Telomerase; RNA component; vaccine; antibody; cancer; EF2H;
 KW nucleolin; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX misc-feature

XX 21

XX /tag= a

XX /note= "Designated 0 in the specification, with 7

XX misc-feature

XX 311..320

XX /tag= b

XX /label= "Template-region"

XX /note= "This region is not further defined in the

XX specification"

XX US6261556-B1.

XX 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

XX 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

PA Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;

PI Kealey JT;

XX WPI; 2001-450477/48.

DR WPI; 2001-450477/48.

XX Purified human telomerase, useful for inducing immune response in

PT animals, comprises several thousand folds increased purity compared

PT with cytoplasmic crude cell preparations -

XX Disclosure; Column 9-12; 29pp; English.

PS The sequence contains human telomerase, hTR, RNA component. The invention

XX relates to a purified human telomerase core enzyme protein comprising

CC 2000-fold increased purity compared with a crude extract of cells from

CC adenovirus-transformed kidney cell line (293 cells) and when associated

CC with telomerase RNA component has DNA polymerase activity and a molecular

CC weight of 200-2000 Kilo Daltons (KDa). The purified telomerase is useful

CC for inducing a humoral or cell-mediated immune response in an animal.

CC Purified telomerase or immunogenic fragments are useful as vaccines for

CC treating diseases associated with over-expression of telomerase, such as

CC cancer and for producing antibodies that recognize telomerase, which are

CC useful as affinity agents in isolating the proteins and for detecting the

CC presence of proteins in a sample, such as cell or tissue. Identification

CC of telomerase aids in diagnosis of cancer or pre-cancerous states.

CC Telomerase and/or telomerase associated proteins are also useful for

CC screening compounds to identify agents that alter the association of

CC telomerase-associated proteins, such as nucleolin or EF2H with

CC telomerase.

XX Sequence 980 BP; 171 A; 303 C; 305 G; 200 T; 1 other;

SQ Query Match 38.4%; Score 333; DB 22; Length 980;

Best Local Similarity 99.7%; Pred. No. 2.3e-96;

Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 593

DB 1 CTGCAGAGATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTCCCGAGCTGGCGAAGGCAACGTCCTTCATG 653

DB 61 TCGGAAGTAAAGACGCAAGCCTTCCCGAGCTGGCGAAGGCAACGTCCTTCATG 120

QY 654 GCCGAAATGGAATTTATTTCCGTCCTCCCAACAGCCCGCGAGAGAGTACTC 713

DB 121 GCCGAAATGGAATTTATTTCCGTCCTCCCAACAGCCCGCGAGAGAGTACTC 180

QY 714 TCACGAGAGCCGCGAGATCAGTCCGCAATCCGTGCGGTGGCGGCGCTCTTAT 773

DB 181 TCACGAGAGCCGCGAGATCAGTCCGCAATCCGTGCGGTGGCGGCGCTCTTAT 240

QY 774 AACCGACTCGCCGCGAGCGCAACGCGGTTGCGGAGGTTGGGCTGGAGGGTGGTGGC 833

DB 241 AACCGACTCGCCGCGAGCGCAACGCGGTTGCGGAGGTTGGGCTGGAGGGTGGTGGC 300

QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGTA 867

DB 301 CATTTTGTCTAACCTTAAGTGAAGGCGTA 334

RESULT 9
 AAD24234
 ID AAD24234 standard; DNA; 981 BP.

XX AAD24234;

XX

```

DT 07-MAR-2002 (first entry)
XX Human telomerase (hTR) gene.
DE Human telomerase (hTR) gene.
XX
XX Human; telomerase; TR; telomerase activity-related disease; therapy;
KM cancer; pregnancy; fertility; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 267..715
FT /tag= a
FT /note= "hTR transcript serves as template in the
FT telomerase ribonucleoprotein"
XX
XX US6300110-B1.
XX
XX 09-OCT-2001.
XX
XX 23-DEC-1998; 98US-0220157.
XX
XX 09-SEP-1995; 95US-003492P.
PR 13-SEP-1996; 96US-0710249.
PR 05-JAN-1996; 96US-0583808.
XX
XX (GERO-) GERON CORP.
XX
XX Villeponteau B, Feng J, Andrews WH, Adams RR;
PI WPI; 2002-033174/04.
XX
XX Peptide products of the human TPC2 and TPC3 gene are involved in
PT regulation of telomere length and activity are useful to diagnose and
PT treat telomere length and activity-related diseases -
XX
XX Example; Fig 9; 60pp; English.
XX
XX The invention relates to methods and reagents for regulating telomere
CC length and for modulating telomerase activity in mammalian cells. The
CC invention also relates to purified, synthetic or recombinant peptides
CC such as TPC2 or TPC3 used for detecting regulators of telomere length
CC and telomerase activity in mammalian cells and for a variety of related
CC diagnostic and therapeutic purposes. The method is useful for screening,
CC diagnosing, monitoring and treating diseases and other conditions such as
CC cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC The present sequence is human telomerase (hTR) gene.
XX
XX Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;
SO

```

```

Query Match 38.4%; Score 333; DB 24; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.3e-96;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 534 CTGCAAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAG 533
DB 1 CTGCAAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAG 60
QY 594 TCGGAGGTAAAGACGCAAGCCTTTCGCGAGCTGCGGAAGGCAAGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCGCGAGCTGCGGAAGGCAAGTCCTTCATG 120
QY 654 GCGGGAATGCAACTTAATTTCCGTTCCGCCCAACCAAGCCGCCCGAGAGAGTACTC 713
DB 121 GCGGGAATGCAACTTAATTTCCGTTCCGCCCAACCAAGCCGCCCGAGAGAGTACTC 180
QY 714 TCACGAGAGCCGCGAGAGTCAGTTGGCCCAATCCGTGCGGCGCGCTTCCTTAT 773
DB 181 TCACGAGAGCCGCGAGAGTCAGTTGGCCCAATCCGTGCGGCGCGCTTCCTTAT 240
QY 774 AAGCCGACTGCGCGAGAGGCAAGCGGTTGCGGAGAGGCTGCGAGAGGTTGGTGGC 833
DB 241 AAGCCGACTGCGCGAGAGGCAAGCGGTTGCGGAGAGGCTGCGAGAGGTTGGTGGC 300

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QY 834 CATTTTGTCTAACCCCTACTAGAGAGCGGTA 867
DB 301 CATTTTGTCTAACCCCTACTAGAGAGCGGTA 334

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RESULT 10
AAT89242
ID AAT89242 standard; DNA; 981 BP.
XX
XX AAT89242;
AC
XX 12-MAY-1998 (first entry)
XX
XX Clone containing hTR sequence.
XX
XX
XX Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KM inhibitor; human telomerase RNA; hTR; ds.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_difference 265..716
FT /tag= a
FT /note= "human telomerase RNA"
XX
XX
XX WO9738013-A1.
XX
XX 16-OCT-1997.
XX
XX 09-APR-1997; 97WO-0505931.
XX
XX 09-APR-1996; 96US-0630019.
XX
XX (GERO-) GERON CORP.
XX
XX Corey D, Norton JC, Platyszek MA, Shay JW, Wright WE;
PI WPI; 1997-512647/47.
XX
XX New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT used to inhibit telomerase, for treating tumours and other
PT proliferative diseases, also for diagnosis
XX
XX Disclosure; Pages 20-21; 76pp; English.
XX
XX
XX This fragment of cloned DNA contains the human telomerase RNA (hTR)
CC sequence, (266-716bp). The hTR region contains a CCC template which
CC the peptide nucleic acid (PNA) can recognise. The presence of a GGG
CC in the PNAs allows for the specific hybridisation to the template
CC region of this hTR component. PNAs can be used as probes to detect the
CC RNA component of mammalian telomerase and as inhibitors of telomerase
CC activity, especially in the treatment of cancer.
XX
XX Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;
SO

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```

Query Match 38.3%; Score 332.4; DB 18; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.6e-96;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 534 CTGCAAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAG 593
DB 1 CTGCAAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAG 60
QY 594 TCGGAGGTAAAGACGCAAGCCTTTCGCGAGCTGCGGAAGGCAAGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCGCGAGCTGCGGAAGGCAAGTCCTTCATG 120
QY 654 GCGGGAATGCAACTTAATTTCCGTTCCGCCCAACCAAGCCGCCCGAGAGAGTACTC 713
DB 121 GCGGGAATGCAACTTAATTTCCGTTCCGCCCAACCAAGCCGCCCGAGAGAGTACTC 180
QY 714 TCACGAGAGCCGCGAGAGTCAGTTGGCCCAATCCGTGCGGCGCGCTTCCTTAT 773

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Db 181 TCACGAGAGCGCGGAGGATGAGCTTGCCCAATCCGTGCGCGCGCCCTCCCTTTAT 240
 QY 774 AAGCCGACTGCGCGGAGCGGACACCGGTTGCGAGGCTGGGCTGGAGGCGTGGTGGC 833
 Db 241 AAGCCGACTGCGCGGAGCGGACACCGGTTGCGAGGCTGGGCTGGAGGCGTGGTGGC 300
 QY 834 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA 867
 Db 301 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA 334

RESULT 11

AA63644 standard; DNA; 981 BP.

AA63644:
 15-FEB-1999 (first entry)
 Human telomerase RNA component sequence from lambda clone 28-1.
 Lambda clone 28-1; human; telomerase RNA component; anticancer therapy;
 assay; vaccine; cancer; purification; ss.

OS Synthetic.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT mISC-feature 266..716
 FT /tag= "human telomerase RNA component sequence"

MO9845450-A1.

15-OCT-1998.

04-APR-1997; 97WO-US06012.

04-APR-1997; 97WO-US06012.

(GERO-) GERON CORP.

Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;
 Vasserot AP, Weinrich SL;

WPI: 1998-594485/50.

Purification of telomerase on affinity material - useful for, e.g.
 diagnosis and treatment of cancer

Disclosure: Pages 14-15; 76pp; English.

The present sequence represents the pStI fragment of the 2.4 kb
 SauIIAI-HindIII fragment of lambda clone 28-1. This clone contains
 human telomerase RNA component gene sequences. The specification
 provides methods for purifying human telomerase. The methods involve
 the use of several sequential steps, including the use of two matrices
 that bind molecules bearing negative charges, a matrix that binds
 molecules bearing positive charges, an affinity purification step
 and a size separation. Telomerase is a particularly target of anticancer
 therapies, and is useful in assays for characterizing (pre)cancerous
 cells. The present sequence can be used for such assays. Telomerase can
 also be used to screen for specific modulators, for biochemical analysis
 of its activity, and in preparation of antibodies. Fragments of
 telomerase, or nucleic acid encoding them, are used in vaccines, and
 for treating over expression of telomerase, particularly in cancer.

Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 38.3%; Score 333.4; DB 19; Length 981;

Best Local Similarity 99.7%; Pred. No. 3,6e-96;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTCGAGAGATAGAAAAAGGCCCTGATACCTCAAGTTAGTTTCACCTTTAAAGAG 593
 Db 1 CTCGAGAGATAGAAAAAGGCCCTGATACCTCAAGTTAGTTTAAAGAG 60
 QY 594 TCGGAAGTAAAGACGCAAAAGCTTTCGAGCTGGCGAAAGGCAACGTCTTCATG 653
 Db 61 TCGGAAGTAAAGACGCAAAAGCTTTCGAGCTGGCGAAAGGCAACGTCTTCATG 120
 QY 654 GCCGGAATGGAACCTTAATTTCCGTTCCCGCAACACGACCCCGGAGAGAGTACATC 713
 Db 121 GCCGGAATGGAACCTTAATTTCCGTTCCCGCAACACGACCCCGGAGAGTACATC 180
 QY 714 TCACGAGAGCGCGGAGAGTACAGCTTGCCCAATCCGTGCGGCGCGCTCTTTAT 773
 Db 181 TCACGAGAGCGCGGAGAGTACAGCTTGCCCAATCCGTGCGGCGCGCTCTTTAT 240
 QY 774 AAGCCGACTGCGCGGAGCGGACACCGGTTGCGAGGCTGGGCTGGAGGCGTGGC 833
 Db 241 AAGCCGACTGCGCGGAGCGGACACCGGTTGCGAGGCTGGGCTGGAGGCGTGGC 300
 QY 834 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA 867
 Db 301 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA.334

RESULT 12

AA23626 standard; DNA; 981 BP.

AA23626:

07-JAN-2000 (first entry)

Human clone 28-1 containing telomerase fragment.

Telomerase; human; immune response; cancer; vaccine; treatment;
 disease; ss.

Homo sapiens.

US5968506-A.

19-OCT-1999.

04-APR-1997; 97US-0833377.

04-AUG-1995; 95US-0510736.

(GERO-) GERON CORP.

Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;
 Vasserot AP;

WPI: 1999-590379/50.

Compositions comprising human telomerase, useful for treating diseases
 associated with overexpression of telomerase e.g. cancer -

Disclosure: Column 41-42; 34pp; English.

This invention describes a novel composition comprising human telomerase
 having at least 2000-fold (preferably at least 60000-fold) increased
 relative purity compared with crude extract of cells from
 adenovirus-transformed kidney cell line. The composition is useful for
 eliciting an immune response in animals and may therefore be used as a
 vaccine for treating diseases associated with the overexpression of
 telomerase e.g. cancer. This sequence represents a nucleic acid fragment
 from human clone 28-1 which contains a fragment of the human telomerase
 described in the method of the invention.

Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;


```
OS Homo sapiens.
XX Key Location/Qualifiers
FH misc_feature 266..716
FT /tag= a
FT /note= "htr gene sequence"
FT misc_feature 311..320
FT /tag= b
FT /note= "Template region of htr used as template for
FT synthesis of telomeric repeats"
XX
XX US6294650-B1.
XX 25-SEP-2001.
XX
XX 08-JUL-1999: 99US-0349532.
XX
XX 09-APR-1997: 97US-0838545.
XX 09-APR-1996: 96US-0630019.
XX
XX (TEXA ) UNIT TEXAS SYSTEM.
XX
XX Shay JW, Wright WE, Platyszek MA, Corey DR, Norton JC;
XX MPI: 2001-638024/73.
XX
XX New peptide nucleic acids that hybridises to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases
XX
XX Disclosure: Column 13-16; 46pp; English.
XX
XX CC The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridising to the RNA component of mammalian
XX telomerase. The PNAs are useful as probes to detect the RNA component
XX of mammalian telomerase and as inhibitors of telomerase activity, or to
XX detect and/or quantitate polynucleotide having the human telomerase
XX RNA component (htr) sequence, as well as in forensic identification of
XX individuals, such as paternity testing or identification of criminal
XX suspects or unknown descendants based on the htr gene RFLP pattern. The
XX PNA can be further used for treating or preventing cancer, inflammation,
XX lymphoproliferative diseases, autoimmune disease, or neurodegenerative
XX diseases. The PNAs in combination with other pharmaceuticals (such as
XX antineoplastic or cytostatic agents) can be used for treating neoplasia,
XX hyperplasia, human immunodeficiency virus (HIV) infections, acquired
XX immunodeficiency syndrome (AIDS) and associated pathologies, and other
XX diseases characterised by abnormal telomere metabolism or telomerase
XX activity. The present sequence represents a PstI fragment, derived
XX from bacteriophage lambda clone 28-1, containing the htr gene sequence.
XX
XX Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other:
XX
XX Query Match 38.3%; Score 332.4; DB 23; Length 981;
XX Best Local Similarity 99.7%; Pred. No. 3,6e-96;
XX Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX 534 CTCGACAGGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 593
XX 1 CTCGAGGGGTTAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
XX
XX 594 TCGGAGTAAGACGCAAAAGCTTTCCCGAGCTGGGAGGAGGCAAGCTCTTCTCATG 653
XX TCGGAGTAAGACGCAAAAGCTTTCCCGAGCTGGGAGGAGGCAAGCTCTTCTCATG 120
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XX 654 GCGGGAATGGAATTTATTTCCCGTCCCGCAACCAAGCCCGCCGAGAGAGTGAATC 713
XX GCGGGAATGGAATTTATTTCCCGTCCCGCAACCAAGCCCGCCGAGAGAGTGAATC 180
XX
XX 714 TCACGAGAGCGCGGAGAGTACCTTGCGCAATCCGTCGGGTGGGCGCCCTCTTTAT 773
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XX
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QY 774 AACCCACTCGCCCGCAGCGACCCGGTTCGCGAGAGGTGGCCCTGGAGGGGTGTGGC 833
DB 241 AACCCAGCTCGCCCGCAGCGACCCGGTTCGCGAGAGGTGGCCCTGGAGGGGTGTGGC 300
QY 834 CATTTTGTCTAACCTTAACCTGAGAGAGGCGCTA 867
DB 301 CATTTTGTCTAACCTTAACCTGAGAGAGGCGCTA 334
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XX RESULT 15
XX AAZ07323
XX ID AAZ07323 standard; DNA; 176 BP.
XX
XX AC AAZ07323:
XX
XX DT 22-OCT-1999 (first entry)
XX
XX DE Human telomerase RNA (htr) proximal promoter (nucleotides -107 to +69).
XX
XX KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; htr;
XX KW gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
XX
XX OS Homo sapiens.
XX
XX PN MO9938964-A2.
XX
XX PD 05-AUG-1999.
XX
XX PF 29-JAN-1999: 99WO-GB00308.
XX PR 29-JAN-1998: 98GB-0001902.
XX
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI Keith WN;
XX
XX DR MPI: 1999-479183/40.
XX
XX PT Mouse and human telomerase RNA gene promoters, useful for tumor
XX specific gene therapy
XX
XX Disclosure: Fig 19; 109pp; English.
XX
XX CC The invention relates to promoter regions from mouse and human telomerase
XX CC RNA (TR) component genes. The TR gene promoter can be linked to a
XX CC heterologous gene, especially a gene encoding a cytotoxin, for therapy
XX CC of cancer, especially neoplasias. The telomerase is necessary for the
XX CC unrestricted proliferative capacity of many human cancers. Mutation or
XX CC dysregulation of the telomerase repression pathway may cause reactivation
XX CC or upregulation of telomerase expression in cancer. Substances
XX CC identified in the methods, can be used to block transcription from the TR
XX CC gene promoter through interaction of the 5' regulatory sequences. These
XX CC substances, e.g. antisense oligonucleotides, transcription factors,
XX CC peptide nucleic acids and factors that disrupt signal transduction, are
XX CC useful for cancer therapy. In particular, gene therapy vectors
XX CC (especially pGR62-codAup) comprising the promoter and a viral thymidine
XX CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
XX CC neoplasia can be controlled or treated. Direct down-regulation of
XX CC telomerase RNA gene through manipulation of transcription factors may be
XX CC effective anticancer therapy and the cloning of the htr gene promoter
XX CC allows the analysis of therapeutic molecules which modulate htr promoter
XX CC activity. The present sequence represents a human TR gene (htr)
XX CC proximal promoter region.
XX
XX SQ Sequence 176 BP; 30 A; 51 C; 63 G; 32 T; 0 other:
XX
XX Query Match 20.3%; Score 176; DB 20; Length 176;
XX Best Local Similarity 100.0%; Pred. No. 2,8e-46;
XX Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 692 AGCCGCGCGAGAGTACTCTACAGAGAGCGCGAGAGTCAAGTTGCGCAATCCGTGC 751
XX
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Db 61 GGTGGGGGGCCGCTCCCTTATATAAGCCGACTCGCCCGGCGAGCGCACCCGGGTTGGGAGGG 120
QY 812 TGGGCTTGGGAGGGGTGTGTGCTTAACCTTAAGTGAAGAGGGCTA 867
Db 121 TGGGCTTGGGAGGGGTGTGTGCTTAACCTTAAGTGAAGAGGGCTA 176

Search completed: January 25, 2003, 14:59:34
job time : 315 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:41:20 : Search time 92 Seconds
(without alignments)
4233.833 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867
Sequence: 1 agctaactagagagcgtgaga.....cctaactagagagcgtgaga 867

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published_Applications_NA.*
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3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	848.6	97.9	2426	10 US-09-057-351-3	Sequence 3, Appl1
2	109.2	12.6	133893	9 US-10-161-510-1	Sequence 1, Appl1
3	101.8	11.7	180216	10 US-09-835-232-6	Sequence 6, Appl1
4	101.2	11.7	32193	10 US-09-764-877-2623	Sequence 2623, Ap
5	101.2	11.7	684973	10 US-09-263-959-1	Sequence 1, Appl1
6	99.6	11.5	302250	10 US-09-962-832-154	Sequence 154, Ap
7	99.2	11.4	9914	9 US-09-764-847-1558	Sequence 1558, Ap
8	99	11.4	31994	9 US-09-764-904-71	Sequence 71, Appl1
9	99	11.4	31994	9 US-09-764-860-599	Sequence 599, Ap
10	98.6	11.4	28897	10 US-09-764-877-3897	Sequence 3897, Ap
11	98	11.3	289	10 US-09-764-877-2732	Sequence 2732, Ap
12	97.6	11.3	2756	10 US-09-764-853-898	Sequence 898, Ap
13	97.4	11.2	27148	10 US-09-764-860-1046	Sequence 1046, Ap
14	97	11.2	10885	10 US-09-764-877-3843	Sequence 3843, Ap
15	96.4	11.1	30625	10 US-09-927-091-5	Sequence 5, Appl1
16	96.4	11.1	32187	10 US-09-764-847-1550	Sequence 1550, Ap
17	96.4	11.1	32193	10 US-09-764-847-1549	Sequence 1549, Ap
18	96.4	11.1	145831	10 US-09-969-708-79	Sequence 79, Appl1
19	96.4	11.1	145831	10 US-09-954-456-2116	Sequence 2116, Ap

C 20	96	11.1	303	10 US-09-764-870-604	Sequence 604, App
C 21	96	11.1	1115	9 US-09-981-353-126	Sequence 126, App
C 22	96	11.1	1545	10 US-09-764-877-3172	Sequence 3172, Ap
C 23	96	11.1	10378	10 US-09-764-847-1616	Sequence 1616, Ap
C 24	96	11.1	10472	10 US-09-764-847-1615	Sequence 1615, Ap
C 25	96	11.1	17752	10 US-09-748-127-3	Sequence 3, Appl1
C 26	96	11.1	32193	9 US-09-764-868-1508	Sequence 1508, Ap
C 27	96	11.1	32193	9 US-09-764-868-1508	Sequence 1508, Ap
C 28	96	11.1	53542	10 US-09-801-574-61	Sequence 61, Appl1
C 29	96	11.1	98865	10 US-09-770-669A-3	Sequence 3, Appl1
C 30	95.8	11.0	2240	10 US-09-814-282-1	Sequence 1, Appl1
C 31	95.6	11.0	423	10 US-09-867-701-7043	Sequence 7043, Ap
C 32	95.4	11.0	36159	12 US-10-135-667-3	Sequence 3, Appl1
C 33	95	11.0	32169	10 US-09-764-887-1963	Sequence 1963, Ap
C 34	95	11.0	32190	10 US-09-764-887-3389	Sequence 3389, App
C 35	94.8	10.9	142	10 US-09-764-877-3240	Sequence 3240, App
C 36	94.8	10.9	4071	10 US-09-764-869-2040	Sequence 2040, App
C 37	94.8	10.9	32195	10 US-09-764-870-611	Sequence 611, App
C 38	94.8	10.9	32195	10 US-09-764-870-617	Sequence 617, App
C 39	94.8	10.9	32195	10 US-09-764-869-1605	Sequence 1605, App
C 40	94.8	10.9	176373	9 US-10-095-407-17	Sequence 17, Appl1
C 41	94.6	10.9	7017	10 US-09-764-877-3773	Sequence 3773, App
C 42	94.6	10.9	8868	10 US-09-803-670-3	Sequence 3, Appl1
C 43	94.6	10.9	20522	10 US-09-764-877-3774	Sequence 3774, App
C 44	94.6	10.9	21470	10 US-09-764-847-1157	Sequence 1157, App
C 45	94.4	10.9	311	9 US-09-860-670-199	Sequence 199, App

ALIGNMENTS

RESULT 1

US-09-057-351-3
Sequence 3, Application US/09057351

Patent No. US20010034439A1

GENERAL INFORMATION:

APPLICANT: Villedonpau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/057,351

FILING DATE: 08-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-000821US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200


```

Oy      1  AGCTACTAGGAGGCTGAGACACGAGATCGTTGAACCCGGGAGCGAGAGTTGCAGTG 60
Db      64485  AGCTACTAGGAGGCTGAGCGACGAGGAATGCTTGAACCCGGGAGCGAGAGTTGCAGTG 64426
Oy      61  AGCCGAGTCAGCGCCACTAGACTCCATCCAGCTGGGGGAAAGAGCAAGACTCCGCTTCA 120
Db      64425  AGCCGAGATCGCCGCGCACATACAC---TTCAGCCTGGGCAACGAGCGAGACTCCGCTTCA 64370
Oy      121  AAAAAAAAAAATCGTTACAA 139
Db      64369  AAAAAAAAAAAGTTATATA 64351

RESULT 4
US-09-764-877-2623/C
; Sequence 2623 Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2623
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-2623

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Query March 11.7%: Score 101.2: DB 10: Length 32193;
Best Local Similarity 86.2%: Pred No.1.5e-19;
Matches 112: Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGGCTGAGACACGAGAAATCGCTTGAACCCGGGAGGACAGAGTTGCAGTG 60
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Db 31984 AGCTACTCTGGAGGCTGAGGACGAGAAATCGCTTGAACCCAGGAGGACAGAGTTACAATG 31925

QY 61 AGCCGAGATCACGCCACCTAGACTCCATCCAGCCTTGGGCGAAGAGCAGACTCCGTCTCA 120
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Db 31924 AGCTGAGATCGGGCCACTGCACTCAGCTCAGCTGGCGCAACAGAGTAAAGACTATCTCA 31865

QY 121 AAAAAAAAAA 130
||||| |||||||
Db 31864 AAAAAAAAAA 31855

RESULT 5
US-09-263-959-1/c
: Sequence 1, Application US/09263959
: Patent No. US20020150891A1
: GENERAL INFORMATION:
: APPLICANT: Hood, Leroy E.
: APPLICANT: Rowen, Lee
: APPLICANT: Koop, Ben F.
: TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTILIZE
: NUMBER OF SEQUENCES: 1279
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/263,959

```

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: FILING DATE: 05-MAR-1999
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Mcmasters, David D.
: REGISTRATION NUMBER: 33,963
: REFERENCE/DOCKET NUMBER: 920010.426C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 664973 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-263-959-1

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Query Match	11.7%	Score 101.2	DB 10	Length 684973
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QY 1	AGCTACTCAGAGAGCGCTGAGACAGCAAGATCGCTTGTAACCCGCGGAGCAGAGAGCTTCAGTG	60		
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QY	61	AGCCGAGATCAAGCCACTAGACTCCATCCAGCTTGCGGAAAGACCAAGACTCCGCTTCA	120	
Db 442741	AGCCGAGATCGCTGCGCACTGCACCTCCATCCAGCTTGCGGAGACAGACGCACTCTCTCA	442682		
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Db 442681	AAAAAAAAAA 442672			

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RESULT 6
US-09-962-832-154/C
; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
; LENGTH: 302250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-154

Query Match          11.5%; Score 99.6; DB 10; Length 302250;
Best Local Similarity 85.4%; Pred. No. 1.5e-18;
Matches 111; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Db 226482  AGCTACTCGGGAGGCTGAGGCGAGAAAGATCGCTTGAACCCGGGAGCGAGCTGCGGTG 226423
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      61  AGCGAGATCAAGCGCATAGACTCCATCCACGCTTGCGGCGAAAGACAGACTCCGTCTCA 120
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Db 226422  AGCGAGATCAACACACACTGTCTCTCGACAGAGACGCTTGCGGCGAAGCGAGACTCCATCTCA 226363
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Db 226362  AAAAAAACA 226353

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Db	8377 AGCCAGATGTTGGCCACGTGCACCTC---CAGCCTGGGTGACAGAGCAGACATCCTGCTCA	8322			
QY	121 AAAAAAAAAATCGTTACATTTATGTGGATTACTCCCTCTTTTAACT	170			
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RESULT 8
US-09-764-904-71/c
; Sequence 71, Application US/09764904
; Patent No. US2002017345A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122
; CURRENT APPLICATION NUMBER: US/09/764,904
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 31994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-904-71

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Query Match Similarity	11.4%	Score 99:	DB 9:	length 31994:
Best Local Similarity	82.0%	Pred. No.	6.8e-19:	
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QY 61	AGCCGAGATCACGCCACTAGACTCCATCCATCCAGCCTTGCGGCGAAGGAGCAAGATCCGCTCTCA 120			
Db 5741	AGCCGAGATGCGACCATTCATTCACCCGAGCGCTGGGCAACAGAGCAAGACTATGCTCTCA 5682			
QY 121	AAAAAAAAAATCTTACAA 139			
Db 5681	AAAAACAAAAACAAAAACAA 5663			

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Best Local Similarity	82.0%	Pred. No. 6,8e-19		
Matches 114	Conservative	0	Mismatches 25	Indels 0
			Gaps	0
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DB 5801	AGTTACTTGGGAGGGCTGAGACAGAGAAATCGCTTGACTCGGGAGGTTGAGGTTGCAGTG	5742		
QY 61	AGCCGAGATCACGCCACTRGAAGCTCCATCCAGGCTTGCGGCGAANAAGACAGACTTCGCTTCA	120		
DB 5741	AGCCGAGATGCGACCATTCGACCCGACGAGCCTGGCGACAGACAGACTATGCTTCA	5682		
QY 121	AAAAAAAAAATCGTTACAA	139		
DB 5681	AAAACAAAAACAAAAACA	5663		

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; RESULT 10
; US-09-764-877-3897/C
; Sequence 3897, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3897
; LENGTH: 28897
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-3897

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	Query Match	Similarity	Best Local	Matches	Conservative	Mismatches	Indels	Gaps
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	63.3%	Pred. No. 8.5e-19;						
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Qy	1	ACTACTCAGGAGGCTGAGACACAGAGATCCCTTTAACC	GGGAGGACAGGTTGCACG	60				
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Qy	61	AGCCGAGATCAGCGCACTAGACTCCATCCAGCTGGCGGCAAAAGACAAACACTCCGTCTCA	120					
Db	9396	AGCCGAGATCCCGCACTGCAC-----TCCAGCGCTGGGCGACAGACGAGACTCCGCTCA	9341					
Qy	121	AAAAAAAAAATCGTTACATTTATGCTGATTCACCTCTTTTAACTCATCAAGACA	180					
Db	9340	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACACTTATTACTTTTAAATAAAGT	9281					
Qy	181	CAGCACTACTTTAAAGCAAGTCAATGATGTGAACGCCCTTTCTTCTTAATAAAGGAG	240					

Db 9280 TAGCTTAGGACCCAGACGACCTGCACGTTTAGATTGTAATTTCTTTCTTTGGGTAACGTGAG 9221

Oy 241 ATTCACTCCTTAAGATTAAATTAATGTAG 267

Db 9220 ATAGCTTTACTGMAAGCAGACACMAAGAA 9194

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: RESULT 11
: US-09-764-877-2732/C
: Sequence 2732, Application US/09764877
: Patent No. US20020147140A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC005
: CURRENT APPLICATION NUMBER: US/09/764,877
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 4031
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2732
: LENGTH: 289
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-764-877-2732

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RESULT 12
US-09-764-853-898/c
: Sequence 898, Application US/09764853
: Patent No. US20020090672A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P1206
: CURRENT APPLICATION NUMBER: US/09/764,853
: PRIORITY FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 939
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 898
: LENGTH: 2756
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-764-853-898

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QY 121 AAAAAAAAAATCGTTACAATTATCG 146
 ||||| | || |
 Db 1665 AAAAAAAAAAAAAAAAAAAAAATCG 1640

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RESULT 13
; US-09-764-860-1046/C
; Sequence 1046, Application US/09764860
; Patent No. US2002094953A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;   FILE REFERENCE: PC008
;   CURRENT APPLICATION NUMBER: US/09/764,860
;   CURRENT FILING DATE: 2001-01-17
;   Prior application data removed - consult PALM or file wrapper
;   NUMBER OF SEQ ID NOS: 1198
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 1046
;   LENGTH: 27148
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (22804)
;   OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-860-1046

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RESULT 14
US-09-764-877-3843
: Sequence 3843 Application US/09764877
: Patent No. US20020147140A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC005
: CURRENT APPLICATION NUMBER: US/09/764,877
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 4031
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 3843
: LENGTH: 10885
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-764-877-3843

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